

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:21:15 ; Search time 11.88 seconds

(without alignments)  
355.255 Million cell updates/sec

Title:

Perfect score: 628  
Sequence: 1 DFGLDCEHSTESRCRCRYPL.....KEQIYKIPAMVDRCGCS 109

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	99.0	375	1	GDF8_CHICK
2	622	99.0	375	1	GDF8_HUMAN
3	622	99.0	375	1	GDF8_MELGA
4	622	99.0	375	1	GDF8_PIG
5	622	99.0	376	1	GDF8_MOUSE
6	622	99.0	376	1	GDF8_MOUSE
7	616	98.1	375	1	GDF8_RAT
8	612	97.5	375	1	GDF8_PAPHA
9	611	97.3	375	1	GDF8_SHEEP
10	574	91.4	405	1	GDF8_BOVIN
11	574	91.4	405	1	GDF8_MOUSE
12	563	89.6	374	1	GDF8_HUMAN
13	527	83.9	345	1	GDF8_BRARE
14	241	38.4	235	1	GDF8_RAT
15	239	38.1	355	1	IHBB_MOUSE
16	236	37.6	391	1	DVRI_BRARE
17	235	37.4	349	1	IHBB_CHICK
18	235	37.4	407	1	IHBB_PIG
19	235	37.4	408	1	IHBB_HUMAN
20	225.5	35.9	207	1	IHBB_BOVIN
21	225.5	35.9	513	1	BMP6_RAT
22	223.5	35.6	510	1	BMP6_HUMAN
23	216.5	34.5	426	1	IHBA_MOUSE
24	212.5	33.8	360	1	IHBA_HORSE
25	211.5	33.7	125	1	DVRI_XENLA
26	211.5	33.7	352	1	IHBC_MOUSE
27	211.5	33.7	436	1	IHBC_MOUSE
28	210.5	33.5	424	1	GDF6_BOVIN
29	210.5	33.5	424	1	IHBA_MOUSE
30	210.5	33.5	424	1	IHBA_PIG
31	210.5	33.5	425	1	IHBA_RAT
32	210.5	33.5	425	1	IHBA_BOVIN
33	210.5	33.5	426	1	IHBA_SHEEP
					BMP7_XENLA

34	210.5	33.5	426	1	IHBA_HUMAN	P08476	homo sapien
35	209.5	33.4	431	1	BMP7_HUMAN	P18075	homo sapien
36	208.5	33.2	352	1	IHBC_HUMAN	P55103	homo sapien
37	207.5	33.0	151	1	GDF7_MOUSE	P43029	mus musculus
38	207.5	33.0	430	1	BMP7_MOUSE	P23359	mus musculus
39	206.5	32.9	495	1	GDF5_MOUSE	P43027	mus musculus
40	206.5	32.9	501	1	GDF5_HUMAN	P43026	homo sapien
41	205.5	32.7	402	1	BMP8_HUMAN	P43820	homo sapien
42	204.5	32.6	350	1	IHBE_MOUSE	O08717	mus musculus
43	204.5	32.6	350	1	IHBE_RAT	O88959	rattus norv
44	204.5	32.6	351	1	IHBC_RAT	O9WUK5	rattus norv
45	204	32.5	350	1	DAF7_CAEEL	P92172	Caenorhabditis

## ALIGNMENTS

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RESULT 1
ID      GDF8_CHICK      STANDARD:      PRT:      375 AA.
AC      0A2220;
DT      15-JUL-1999 (Rel. 38, Created)
DT      15-JUL-1999 (Rel. 38, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN      GDF8 OR MSTN.
OS      Gallus gallus (chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=WHITE LEGHORN; TISSUE=Skeletal muscle;
RX      MEDLINE=98024153; PubMed=9356471;
RA      McPherron A.C., Lee S.-J.;
RT      "Double muscling in cattle due to mutations in the myostatin gene.";
RL      Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC      -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC      -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: AF019621; AAB86688.1; -
DR      HSSP: P18075; BMP.
DR      InterPro: IPR001839; TGF-beta.
DR      InterPro: IPR001111; TGF-beta.
DR      Pfam: PF00019; TGF-beta. 1.
DR      Pfam: PF00688; TGF-beta. 1.
DR      ProDom: PD000357; TGF-beta. 1.
DR      SMART: SM00204; TGF-beta. 1.
DR      PROSITE: PS00250; TGF-BETA_1; 1.
KW      Growth factor; Cytokine; Glycoprotein; Signal.
FT      SIGNAL      1      23
FT      PROPEP      24      266
FT      CHAIN      267      375
FT      DISULFID      281      340
FT      DISULFID      309      372
FT      DISULFID      313      374
FT      DISULFID      339      339
FT      CARBOHYD      71      71
SO      SEQUENCE      375 AA; 42707 MW; DA732DB9426E4DAF CRC64;
Query Match      99.0%; Score 622; DB 1; Length 375;

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	Best Local Similarity	99.1%	Pred. No. 4e-63:		Mismatches	1:	Indels	0:	Gaps	0:
Oy	1	DFGLDCDEHSTESRCRCRYPLTVDFEAFGDMWIIAPKRYKANYCSCGCEFEVLQKYPHTL	60							
Db	267	DFGLDCDEHSTESRCRCRYPLTVDFEAFGDMWIIAPKRYKANYCSCGCEFEVLQKYPHTL	326							
Oy	61	VHOANPRGASGRCCTPTLMSPINMLYNGKEQIITGKIPAMVDRCGCS	109							
Db	327	VHOANPRGASGRCCTPTLMSPINMLYNGKEQIITGKIPAMVDRCGCS	375							
RESULT	2									
GDF8_HUMAN		STANDARD:	PRT;	375	AA.					
ID	GDF8_HUMAN	014793;								
DT	15-JUL-1999	(Rel. 38, Created)								
DT	15-JUL-1999	(Rel. 38, Last sequence update)								
DT	01-MAR-2002	(Rel. 41, Last annotation update)								
DE	Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).									
GN	GDF8 OR MSTN.									
OS	Homo sapiens (Human).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.									
OX	NCBI_Taxid=9606;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RP	TISSUE=Skeletal muscle;									
RX	MEDLINE=98024153; PubMed=9356471;									
RA	McPherron A.C., Lee S.-J.;									
RL	"Double muscling in cattle due to mutations in the myostatin gene.,"									
RL	Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).									
RP	[2]									
RP	SEQUENCE FROM N.A.									
RP	TISSUE=Muscle;									
RX	MEDLINE=99061972; PubMed=984394;									
RA	Gonzalez-Cadavid N.F., Taylor W.E., Yarasheski K., Sinha-Hikim I.,									
RA	Ma K., Ezzat S., Shen R., Lalani R., Asa S., Mantla M., Nair G.,									
RA	Atver S., Bhasin S.;									
RT	"Organization of the human myostatin gene and expression in healthy									
RT	men and HIV-infected men with muscle wasting.,"									
RL	Proc. Natl. Acad. Sci. U.S.A. 95:14938-14943(1998).									
CC	-1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL									
CC	MUSCLE GROWTH.									
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).									
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.									
CC	-----									
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).									
CC	-----									
DR	EMBL; AF019627; AAB86694.1; -									
DR	EMBL; AF104922; AAC96327.1; -									
DR	HSSP; P18075; IBMP.									
DR	MIM; 601788; -									
DR	InterPro: IPR001839; TGF-beta.									
DR	InterPro: IPR001111; TGF-beta.									
DR	Pfam; PF00019; TGF-beta; 1.									
DR	Pfam; PF00688; TGF-beta; 1.									
DR	ProDom; PD000357; TGF-beta; 1.									
DR	SMART; SM00204; TGF-beta; 1.									
DR	SMART; PS00250; TGF-beta; 1.									
KW	Growth factor; Cytokine; Glycoprotein; Signal.									

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FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

Query Match 99.0%; Score 622; DB 1; Length 375;
Best Local Similarity 99.1%; Pred. No. 4e-63;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGLDCDEHSTESRCRRPYLTVDFEAFGDMWIIARRRYKANYSCSECEFFVLQKKYPHTL 60
DB 267 DGLGDCDEHSTESRCRRPYLTVDFEAFGDMWIIARRRYKANYSCSECEFFVLQKKYPHTL 326
QY 61 VQANPRGSAGPCCTPTLMSPIINMLYFNGKEIITGKIPAMVYDRCGS 109
DB 327 VQANPRGSAGPCCTPTKNSPIINMLYFNGKEIITGKIPAMVYDRCGS 375

RESULT 3
GDF8_MELGA STANDARD; PRT; 375 AA.
AC 042221;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
GN GDF8 OR MSTN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RS TISSUE=Skeletal muscle;
RA MEDLINE=98024153; PubMed=9356471;
RX McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -! FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -! SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC CC EMBL; AF019625; AAB86692.1; ALT_INIT.
CC DR HSSP; P18075; 1BMP.
CC DR InterPro: IPR001839; TGF-beta.
CC DR InterPro: IPR001111; TGFb_N.
CC DR Pfam; PF00019; TGF-beta.1.
CC DR Pfam; PF00688; TGFb_propeptide.1.
CC DR ProDom; PD000357; TGF-beta.1.
CC DR SMART; SM00204; TGFb.1.
CC DR PROSITE; PS00250; TGF_BETA.1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
KW SIGNAL 1 23
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.
FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 42784 MW; D2AEAB732AEBA4E77 CRC64;

Query Match 99.0%; Score 622; DB 1; Length 375;

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FT CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 375 AA; 42688 MW; 7B49B90KACAB926EA CRC64;

Query Match 98.1%; Score 616; DB 1; Length 375;  
Best Local Similarity 98.2%; Pred. No. 1,9e-62;  
Matches 107; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 60  
DB 267 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 326

QY 61 VHOANPRGSAGPCTPTPLMSPINMLYNGKEQIIYGIKIPAMVYDRGCS 109  
DB 327 VHOANPRGSAGPCTPTPLMSPINMLYNGKEQIIYGIKIPAMVYDRGCS 375

RESULT 8  
ID GDF8\_SHEEP STANDARD; PRT; 375 AA.

AC 018830;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
GN GDF8 OR MSTN.

OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
NCBI\_TaxID=9940;

RP SEQUENCE FROM N.A.  
RC TISSUE-Skeletal muscle;  
RX MEDLINE=98024153; PubMed=9356471;

RA McPherron A.C., Lee S.-J.;  
RT "Double muscling in cattle due to mutations in the myostatin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
MUSCLE GROWTH.

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC -----  
CC EMBL: AF019622; AAB86689.1; -  
CC HSSP: P12643; 3BMP.

DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGF-beta\_N.

DR Pfam: PF00688; TGF-beta; 1.  
DR Pfam: PF00688; TGF-beta; 1.

DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-beta; 1.  
KW Growth factor; Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 23 POTENTIAL.  
FT PROPEP 24 266 POTENTIAL.

FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.  
FT DISULFID 281 340 BY SIMILARITY.

FT DISULFID 309 372 BY SIMILARITY.  
FT DISULFID 313 374 BY SIMILARITY.

FT DISULFID 339 339 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 48 48 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).

SQ SEQUENCE 375 AA; 42827 MW; 1C36F383BB11241 CRC64;

Query Match 97.5%; Score 612; DB 1; Length 375;  
Best Local Similarity 96.3%; Pred. No. 5.5e-62;  
Matches 105; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 60  
DB 267 DFGDCDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANVCSGCEFEFLQKYPHTL 326

QY 61 VHOANPRGSAGPCTPTPLMSPINMLYNGKEQIIYGIKIPAMVYDRGCS 109  
DB 327 VHOANPRGSAGPCTPTPLMSPINMLYNGKEQIIYGIKIPAMVYDRGCS 375

RESULT 9  
ID GDF8\_BOVIN STANDARD; PRT; 375 AA.

AC 018836; 018829;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).  
GN GDF8 OR MSTN OR MH.

OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
NCBI\_TaxID=9913;

RP SEQUENCE FROM N.A., AND VARIANT MH TYR-313.  
RC STRAIN-FRIESIAN; TISSUE-Muscle, and Embryo;  
RX MEDLINE=97458167; PubMed=9314496;

RA Kamadur R., Sharma M., Smith T.P.L., Bass J.J.;  
RT "Mutations in myostatin (GDF8) in double-muscled Belgian Blue and  
RT Piedmontese cattle.";  
RL Genome Res. 7:910-916(1997).

RP SEQUENCE FROM N.A., AND VARIANTS MH LEU-94 AND TYR-313.  
RC STRAIN-HOLSTEIN; TISSUE-Skeletal muscle;  
RX MEDLINE=98024153; PubMed=9356471;

RA McPherron A.C., Lee S.-J.;  
RT "Double muscling in cattle due to mutations in the myostatin gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).

CC -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL  
MUSCLE GROWTH.

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING AND ADULT  
SKELETAL MUSCLE. HIGHEST LEVELS FOUND IN THE HINDLIMB MUSCLES

CC M.SEMIMEMBRANOSUS AND M.BICEPS FEMORIS; LOW LEVELS IN OTHER  
CC HINDLIMB MUSCLES.

CC -1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED THROUGHOUT DEVELOPMENT.  
CC DAY 31 UP UNTIL LATE GESTATION.

CC -1- DISEASE: DEFECTS IN GDF8 ARE THE CAUSE OF THE DOUBLE-MUSCLE  
PHENOTYPE OR MUSCULAR HYPERTROPHY (MH), AN AUTOSOMAL RECESSIVE  
DISEASE FREQUENTLY FOUND IN THE BELGIAN BLUE AND PIEDMONTSE  
CATTLE BREEDS. THIS DISEASE IS CHARACTERIZED BY AN INCREASED  
NUMBER OF MUSCLE FIBERS (HYPERPLASIA), RESULTING IN AN INCREASE IN  
MUSCLE MASS OF 20-25%.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC -----

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CC EMBL: AF019621; AAB81508.1; -  
CC HSSP: P18075; 1BMP.

DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGF-beta\_N.

DR InterPro: IPR001111; TGF-beta\_N.

DR Pfam: PF00019; TGF-beta: 1.  
 DR Pfam: PF00688; TGF-beta: 1.  
 DR Pfam: PF000357; TGF-beta: 1.  
 DR SMART: SM00204; TGF-beta: 1.  
 DR PROSITE: PS00250; TGF-beta: 1.  
 KW Growth factor; Cytokine; Glycoprotein; Signal; Disease mutation.  
 FT SIGNAL 1 18  
 FT PROPEP 19 266  
 FT CHAIN 267 375  
 FT DISULFID 281 340  
 FT DISULFID 309 372  
 FT DISULFID 313 374  
 FT DISULFID 339 374  
 FT CARBOHYD 47 47  
 FT CARBOHYD 71 71  
 FT VARIANT 94 94  
 FT VARIANT 313 313  
 FT CONFLICT 14 14  
 SO SEQUENCE 375 AA; 42520 MW; E1B791AD92D4A9E6 CRC64;

Query Match 97.3%; Score 611; DB 1; Length 375;  
 Best Local Similarity 97.2%; Pred. No. 7,1e-62;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 60  
 DB 267 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 326  
 QY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEIITGKIPAMVVDRCGS 109  
 DB 327 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEIITGKIPAMVVDRCGS 375

RESULT 10  
 GDFB\_MOUSE STANDARD: PRT: 405 AA.  
 AC 0921W4; Q90X55; Q9R221;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).  
 GN GDF11 OR BMP11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99177155; PubMed=10075854;  
 RA Ganer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;  
 RA "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in Xenopus embryos."  
 RT Dev. Biol. 208:222-232(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=129/SVJ;  
 RC MEDLINE=99318097; PubMed=10391213;  
 RA McPherron A.C., Lawler A.M., Lee S.-I.;  
 RA "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11."  
 RT Nat. Genet. 22:260-264(1999).  
 RL [3]  
 RP SEQUENCE OF 75-405 FROM N.A.  
 RA MEDLINE=99173787; PubMed=10072786;  
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;  
 RA "Expression of growth/differentiation factor 11, a new member of the BMP/TGF-beta superfamily during mouse embryogenesis."  
 RT Mech. Dev. 80:185-189(1999).  
 RL [4]  
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL  
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD, INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT DENTAL PULP AND BRAIN.  
 CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM, RETINA AND SPECIFIC REGIONS OF THE BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----

CC EMBL: AF100906; AAC72853.1; -;  
 CC EMBL: AF100904; AAC72853.1; JOINED.  
 CC EMBL: AF100905; AAC72853.1; JOINED.  
 CC EMBL: AF028337; AAF21633.1; -;  
 CC EMBL: AF028335; AAF21633.1; JOINED.  
 CC EMBL: AF028336; AAF21633.1; JOINED.  
 CC EMBL: AF092734; AAD05267.1; -;  
 CC HSSP: P18075; IBMP.  
 CC MGD: MGI:1338027; Gdf11.  
 CC InterPro: IPR001839; TGF-beta.  
 CC InterPro: IPR001111; TGF-beta.  
 CC Pfam: PF00019; TGF-beta: 1.  
 CC Pfam: PF00688; TGF-beta: 1.  
 CC ProDom: PD000357; TGF-beta: 1.  
 CC SMART: SM00204; TGF-beta: 1.  
 CC PROSITE: PS00250; TGF-beta: 1.  
 KW Growth factor; Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 296  
 FT CHAIN 297 405  
 FT DOMAIN 29 405  
 FT DOMAIN 29 405  
 FT DISULFID 311 370  
 FT DISULFID 339 402  
 FT DISULFID 343 404  
 FT DISULFID 369 369  
 FT CARBOHYD 92 92  
 FT CARBOHYD 75 75  
 FT CONFLICT 171 171  
 FT CONFLICT 171 171  
 SO SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;

Query Match 91.4%; Score 574; DB 1; Length 405;  
 Best Local Similarity 89.0%; Pred. No. 1.2e-57;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 60  
 DB 297 NFGDGDHSTESRCRCRYPLTVDFEAFGMDWIIAPRRYKANCSCGCEVFLOKYPHTL 356  
 QY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEIITGKIPAMVVDRCGS 109  
 DB 357 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEIITGKIPAMVVDRCGS 405

RESULT 11  
 GDFB\_HUMAN STANDARD: PRT: 407 AA.  
 AC 095390; Q9UID2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).  
 GN GDF11 OR BMP11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99177155; PubMed=10075854;  
 RA Ganer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R., Rosen V.;  
 RA "A novel BMP expressed in developing mouse limb, spinal cord, and tail bud is a potent mesoderm inducer in Xenopus embryos."  
 RT Dev. Biol. 208:222-232(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=129/SVJ;  
 RC MEDLINE=99318097; PubMed=10391213;  
 RA McPherron A.C., Lawler A.M., Lee S.-I.;  
 RA "Regulation of anterior/posterior patterning of the axial skeleton by growth/differentiation factor 11."  
 RT Nat. Genet. 22:260-264(1999).  
 RL [3]  
 RP SEQUENCE OF 75-405 FROM N.A.  
 RA MEDLINE=99173787; PubMed=10072786;  
 RA Nakashima M., Toyono T., Akamine A., Joyner A.;  
 RA "Expression of growth/differentiation factor 11, a new member of the BMP/TGF-beta superfamily during mouse embryogenesis."  
 RT Mech. Dev. 80:185-189(1999).  
 RL [4]  
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.

DE	16-OCT-2001 (Rel. 40, Created)
DE	16-OCT-2001 (Rel. 40, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	growth/differentiation factor 11 precursor (Bone morphogenetic protein 11).
GN	GDF11 OR BMP11.
OS	Homo sapiens (Human).
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_TaxID=9606;
RA	[1]
RA	SEQUENCE FROM N.A.
RP	TISSUE=Fetal brain;
RC	MEDLINE=99177155; PubMed=10075854;
RX	Ganer L.W., Wolman N.M., Celeste A.J., Hattersley G., Hewick R.,
RA	Rosen V.;
RT	"A novel BMP expressed in developing mouse limb, spinal cord, and tail
RT	bud is a potent mesoderm inducer in Xenopus embryos.";
RL	Dev. Biol. 208:222-232(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99318097; PubMed=10391213;
RA	McPherron A.C., Lawler A.M., Lee S.-J.;
RT	"Regulation of anterior/posterior patterning of the axial skeleton by
RT	growth/differentiation factor 11.";
RL	Nat. Genet. 22:260-264(1999).
CC	-1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC	IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC	PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC	TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Secreted (Probable).
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).
CC	-----
DR	EMBL: AF100907; AAC72852.1; -
DR	EMBL: AF028333; AAF21630.1; -
DR	EMBL: AF028334; AAF21631.1; -
DR	HSSP: P18075; 1BMP.
DR	MIM: 603936; -
DR	InterPro: IPR001839; TGF-beta.
DR	InterPro: IPR001111; TGFb.N.
DR	Pfam: PF00019; TGF-beta; 1.
DR	Pfam: PF00688; TGFb.propeptide; 1.
DR	ProDom: PD000357; TGF-beta; 1.
DR	SMART: SM00204; TGFb; 1.
DR	PROSITE: PS00250; TGF-BETA_1; 1.
DR	Prosite: Cytokine; Glycoprotein; signal.
FW	Growth factor; Cytokine; Glycoprotein; signal.
FT	SIGNAL
FT	PROPEP
FT	CHAIN
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FO	SEQUENCE
FO	407 AA: 45090 MW; E8FF48E3635BA8 C6C64; N-LINKED (GLCNAC... ) (POTENTIAL).

Query Match 91.4%; Score 574; DB 1; Length 407;  
 Best Local Similarity 89.0%; Pred. No. 1.2e-57;  
 Matches 97; Conservative 7; Mismatches 5; Indels 0;  
 Gaps 0

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Db      299  NGLGDCDEHSSRCCRIPLYVDFEAFGMDWIIARIVANCSQCEMFQKTPHTL 358
QY      61  VQANPRCSAGCPCPTLTMSPINMLYFNKGEOIYIGKIPAMVYDRCGS 109
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      359  VQANPRCSAGCPCPTLTMSPINMLYFNKGEOIYIGKIPAMVYDRCGS 407

RESULT 12
GDF8_BRARE
ID      GDF8_BRARE      STANDARD:      PRT:      374 AA.
AC      042222:
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAR-2000 (Rel. 39, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Growth/differentiation factor 8 precursor (GDF-8) (Myostatin).
DE      GDF8 OR MSTN.
OS      Brachydanio rerio (zebrafish) (zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
OC      Cypriniformes; Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skkeletal muscle;
RX      MEDLINE=98024153; PubMed=9356471;
RA      McPherron A.C., Lee S.-J.;
RT      "Double muscling in cattle due to mutations in the myostatin gene.";
RT      Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC      -1- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC      MUSCLE GROWTH.
CC      -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF019626; AAB86693.1; -.
DR      HSSP; P12643; 3BMP.
DR      ZFIN; ZDB-GENE-990415-165; gdf8.
DR      InterPro: IPR001839; TGF-beta.
DR      InterPro: IPR001111; TGFb_N.
DR      Pfam; PF00019; TGF-beta; 1.
DR      Pfam; PF00688; TGFb_propeptide; 1.
DR      ProDom; PD000357; TGF-beta; 1.
DR      SMART; SM00204; TGFb; 1.
DR      PROSITE; PS00250; TGF-BETA.1; 1.
KW      Growth factor; Cytokine; Glycoprotein; Signal.
FT      SIGNAL          1      22      POTENTIAL.
FT      PROPEP          23      265      POTENTIAL.
FT      CHAIN           266      374      GROWTH/DIFFERENTIATION FACTOR 8.
FT      DISULFID        280      339      BY SIMILARITY.
FT      DISULFID        308      371      BY SIMILARITY.
FT      DISULFID        312      373      BY SIMILARITY.
FT      DISULFID        338      338      INTERCHAIN (BY SIMILARITY).
FT      CARBOHYD        72      72      N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT      CARBOHYD        274      274      N-LINKED (GLCNAC. . . ) (POTENTIAL).
SO      SEQUENCE        374 AA; 42060 MW; 6302B6C63652576 CRC64;

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Query Match 89.6%; Score 563; DB 1; Length 374;  
 Best Local Similarity 87.2%; Pred. No. 1, 9e-56;  
 Matches 95; Conservative 11; Mismatches 3; Indels 0; Gaps 0.





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FT CHAIN 141 255 INHIBIN BETA B CHAIN.
FT DISULFID 144 152 BY SIMILARITY.
FT DISULFID 151 220 BY SIMILARITY.
FT DISULFID 180 252 BY SIMILARITY.
FT DISULFID 184 254 BY SIMILARITY.
FT DISULFID 219 219 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 135 135 H -> D (IN REF. 2).
SQ SEQUENCE 255 AA; 29178 MW; 2524B21DC648D9A9 CRC64;

Query Match 38.4%; Score 241; DB 1; Length 255;
Best Local Similarity 42.4%; Pred. No. 4e-20;
Matches 50; Conservative 17; Mismatches 37; Indels 14; Gaps 6;

OY 3 GLDDEHSTESRCRCRYPLTVDFEAFGW-DWIIAPRRYKANCSCGECEVFLOKYPHTH-----LVH 62
DB 141 GLEDGRT--SLCCROGFIDFRIGNNDWIIAPRTGYIGNCEBSCP-AVLAVPGSASS 197
57 -HRLVHQANPRG-SAGP---CCTPTLMSPIIMLYFNKGEQIIYKIPAMVYDRGCS 109
DB 198 FHFAVAVQYMRGLNPGVNVSCIPTKLSSMSMLYFDEDEVNIIVRDVPMIVVECGCA 255

RESULT 15
DVR1_BRAE STANDARD; PRT; 355 AA.
AC P35621;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE DVR-1 protein precursor.
GN VGI OR DVR1 OR DVR-1.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=94009920; PubMed=8405668;
RA Heide K.A., Grunwald D.J.;
RT "The DVR-1 (Vg1) transcript of zebrafish is maternally supplied and
RT distributed throughout the embryo."
RL Dev. Biol. 159:418-426(1993).
CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC -1- SUBUNIT: HOMODIMER (PROBABLY).
CC -1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
CC DISTRIBUTED AMONG ALL BLASTOMERES.
CC -1- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
CC GASTRULA.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U00931; AAC27347.1; -.
DR HSSP; P12643; 3BP.
DR ZFIN; ZDB-GENE-980526-389; dvr1.
DR InterPro; IPR002400; GF_cysknut.
DR InterPro; IPR001839; TGF-beta.
DR InterPro; IPR001111; TGF-beta.
DR Pfam; PF00019; TGF-beta; 1.

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DR Pfam; PF00688; TGF-beta; propeptide; 1.
DR PRINTS; PR00438; GFCYSKNUT.
DR PRODOM; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGBB; 1.
DR PROSITE; PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; signal.
FT SIGNAL 1 15
FT PROPEP 16 240
FT CHAIN 241 355
FT DISULFID 254 320
FT DISULFID 283 352
FT DISULFID 287 354
FT DISULFID 319 319
FT CARBOHYD 108 108
FT CARBOHYD 179 179
FT CARBOHYD 296 296
SQ SEQUENCE 355 AA; 40201 MW; 0BD5B9830EBFB222 CRC64;

Query Match 38.1%; Score 239; DB 1; Length 355;
Best Local Similarity 43.4%; Pred. No. 9.5e-20;
Matches 46; Conservative 16; Mismatches 36; Indels 8; Gaps 3;

OY 11 TESRCR-YPLTVDFEAFGW-DWIIAPRRYKANCSCGECEVFLOKYPHTH-----LVH 62
DB 249 TFSNVCKPRRLYLIDPKDVGQMDWIIAPQGYLANVCHGCPFLSLNGTNNHAIQLTVH 308

OY 63 QANRGSGAPCCTPTLMSPIIMLYFNKGEQIIYKIPAMVYDRGCG 108
DB 309 SFDPRGTPQPCVPIKISPIISMLYDNDNVVLRHYEDMVYDECGC 354

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Search completed: May 20, 2002, 09:24:50  
 Job time: 215 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:50 ; Search time 24.89 Seconds  
(without alignments)  
757.591 Million cell updates/sec

Title: US-09-754-826-2  
Perfect score: 628  
Sequence: 1 DFGDDEHSTESRCRPL.....KEQIIVKIPAMVDRGCS 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp Unclassified:\*  
15: sp\_rv1rus:\*  
16: sp\_bacteriap:\*  
17: sp\_patchap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	99.0	162	6	09TSY2
2	622	99.0	375	6	09GMS7
3	622	99.0	375	6	09S086
4	617	98.2	375	13	098SP0
5	611	97.3	375	6	095M97
6	599	95.4	185	6	095N11
7	592	94.3	185	6	09M718
8	563	89.6	389	13	090Y10
9	560	89.2	385	13	090W05
10	557	88.7	373	13	09DD18
11	557	88.7	373	13	090ZD2
12	557	88.7	373	13	090ZD1
13	557	88.7	376	13	098TR4
14	557	88.7	376	13	090WC9
15	557	88.7	376	13	090WC8
16	556	88.5	373	13	090W17

17	555	88.4	376	13	090W06	090W06 umbrina cfr
18	552	87.9	377	13	098TR3	098TR3 morone chry
19	550	87.6	373	13	098UB3	098UB3 salvelinus
20	547	87.1	96	13	09W759	09W759 calina mos
21	522	83.1	107	6	09BGS4	09BGS4 sus scrofa
22	394	62.7	78	6	09XS86	09XS86 equus caball
23	311	49.5	191	13	098TR4	098TR4 perca flave
24	302	48.1	104	13	090Z79	090Z79 ictalurus p
25	294.5	46.9	598	5	09XZ62	09XZ62 drosophila
26	294.5	46.9	598	5	09YAF4	09YAF4 drosophila
27	286	45.5	58	6	095MF3	095MF3 sus scrofa
28	247	39.3	370	13	091350	091350 xenopus lae
29	238	37.9	395	13	09PWG6	09PWG6 anquilla ja
30	234.5	37.3	115	13	09DGE9	09DGE9 cyprinus ca
31	234.5	37.3	393	13	090Z61	090Z61 brachydanto
32	233.5	37.2	392	13	09PMR8	09PMR8 carassius a
33	232.5	37.0	115	13	09DGF1	09DGF1 cyprinus ca
34	232.5	37.0	115	13	09DGE6	09DGE6 oryzias lat
35	232.5	37.0	115	13	09DGE6	09DGE6 brachydanto
36	229.5	36.5	138	13	09MGT9	09MGT9 xenopus lae
37	229.5	36.5	354	13	09YGV1	09YGV1 xenopus lae
38	226.5	36.1	349	5	097138	097138 brugia mala
39	223.5	35.6	361	5	096504	096504 branchiosto
40	223.5	35.6	411	5	09U418	09U418 brachisto
41	222	35.4	373	13	090723	090723 gallus gall
42	222	35.4	373	13	098950	098950 gallus gall
43	216.5	34.5	399	13	09W753	09W753 xenopus lae
44	215.5	34.3	294	6	09BDM9	09BDM9 macaca fasc
45	215.5	34.3	447	6	09BDW8	09BDW8 cercopithec

#### ALIGNMENTS

RESULT 1  
ID 09TSY2 PRELIMINARY; PRT: 162 AA.  
AC 09TSY2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MROSTVITIN (FRAGMENT).  
GN MSTN.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20078370; PubMed=10612246;  
RA Stratil A., Kopecky M.;  
RT "Genomic organization, sequence and polymorphism of the porcine  
RT myostatin (GFET; MSTN) gene."  
RL Anim. Genet. 30:468-470(1999).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AJ237920; CAB40844.1; .  
DR HSSP: P18075; 1BMP.  
DR InterPro: IPR002400; GF\_cysknot.  
DR InterPro: IPR001839; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR PRODOM: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KW Glycoprotein.  
FT NON\_TER 1  
SQ SEQUENCE 162 AA; 18290 MW; FE3535334512856E CRC64;

Query Match 99.0%; Score 622; DB 6; Length 162;  
Best Local Similarity 99.1%; Pred. No. 4.1e-67;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 60
    |||||||
DB 54 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 113
    |||||||
OY 61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
    |||||||
DB 114 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 162

RESULT 2
O9GM97 PRELIMINARY: PRT: 375 AA.
AC O9GM97:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
GN MSN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
NN [1]
NC SEQUENCE FROM N.A.
RC STRAIN=THROUGHERED.
RA Hosoyama T., Yamamouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
RT myostatin in horse.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; AB033541; BAB16046.1; -.
DR HSSP; P18075; BMP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;
```

Query Match 99.0%; Score 622; DB 6; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1e-66;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 326
    |||||||
61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
    |||||||
327 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375
```

```
RESULT 3
O95J86 PRELIMINARY: PRT: 375 AA.
AC O95J86:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
NN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GASTROCNEMIIUS;
```

```
RA Smock S.L., Owen T.A.;
RT "Cloning of the open reading frame DNA for macaque fascicularis
RT (Cynomolgus macaque) myostatin (GDF8).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055750; AAL17640.1; -.
SQ SEQUENCE 375 AA; 42722 MW; 2149B46ACTD446E7 CRC64;
```

Query Match 99.0%; Score 622; DB 6; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1e-66;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 326
    |||||||
OY 61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
    |||||||
DB 327 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375
```

```
RESULT 4
O98SP0 PRELIMINARY: PRT: 375 AA.
AC O98SP0:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
GN MSN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
NN [1]
NC SEQUENCE FROM N.A.
RA Zhang Y., Yang W., Zhu D.;
RT "Genomic structure and expression of the chicken GDF-8 during
RT development.";
```

```
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC EMBL; AF346599; AAK18000.1; -.
DR HSSP; P18075; BMP.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb.N.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; TGF-beta; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 375 AA; 42717 MW; D980E286426E4DAF CRC64;
```

Query Match 98.2%; Score 617; DB 13; Length 375;  
Best Local Similarity 98.2%; Pred. No. 4e-66;  
Matches 107; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 60
    |||||||
DB 267 DGLDCDEHSTESRCCRPPLTVDFEAFGMDWIIAPRKRYKANYCSGCECFVFLQKYPHTHL 326
    |||||||
61 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 109
    |||||||
327 VHOANPRGSAGPCCTPTLMSPINMLYFNKGKEQIITGKIPAMVVDRCGCS 375
```

```
RESULT 5
O95N97 PRELIMINARY: PRT: 375 AA.
AC O95N97:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSTATIN.
GN MSN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
NN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GASTROCNEMIIUS;
```

AC Q95N97;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MYOSTATIN.  
 GN GDF8.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-2143337; PubMed-11451380;  
 RA Jeanplong F., Sharma M., Somers W.G., Bass J.J., Kambadur R.;  
 RT "Genomic organization and neonatal expression of the bovine myostatin  
 gene.";  
 RT Mol. Cell. Biochem. 220:31-37(2001).  
 EMBL; AF320998; AAG48116.1; -  
 SQ SEQUENCE 375 AA; 42551 MW; 84ELAB20650C05F6 CRC64;

Query Match 97.3%; Score 611; DB 6; Length 375;  
 Best Local Similarity 97.2%; Pred. No. 2.1e-65;  
 Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 60  
 DB 267 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 326  
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 109  
 DB 327 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 375

RESULT 6  
 Q95N11 PRELIMINARY; PRT; 185 AA.  
 AC Q95N11;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MYOSTATIN (FRAGMENT).  
 GN MSTN.  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lian Z., Pan Q., Chen H., Jin H., Li N.;  
 RT "Cloning of intron 2 of the myostatin gene in goat.";  
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY032689; AAK49790.1; -  
 FT NON\_TER 1 185  
 FT SEQUENCE 185 AA; 20953 MW; 03675B386E9D4D4 CRC64;

Query Match 95.4%; Score 599; DB 6; Length 185;  
 Best Local Similarity 96.3%; Pred. No. 2.8e-64;  
 Matches 103; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 60  
 DB 79 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 138  
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 107  
 DB 139 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 185

RESULT 7  
 Q9MZ18 PRELIMINARY; PRT; 185 AA.  
 AC Q9MZ18;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MYOSTATIN (FRAGMENT).  
 GN MSTN.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lian Z., Jin H., Li N.;  
 RT "Cloning of intron 2 of the myostatin gene in sheep.";  
 RT Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL; AF266758; AAF78069.1; -  
 DR HSSP; P12643; 3BMP.  
 DR InterPro; IPR001839; TGF-beta.  
 DR Pfam; PF00019; TGF-beta; 1.  
 DR ProDom; PD000357; TGF-beta; 1.  
 DR SMART; SM00204; TGF-beta; 1.  
 DR PROSITE; PS00250; TGF-BETA; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 185  
 FT SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 94.3%; Score 592; DB 6; Length 185;  
 Best Local Similarity 95.3%; Pred. No. 1.9e-63;  
 Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 60  
 DB 79 DFGDDEHSTESRCRYPITVDFAFGWMIAPKRYKANKYSGCEEFYFLOKYPHTL 138  
 OY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 107  
 DB 139 VHOANPRGSAGPCCPTPLMSPINMLYFNKGEQIITYGKIPAMVYDRGC 185

RESULT 8  
 Q90Y0 PRELIMINARY; PRT; 389 AA.  
 AC Q90Y0;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE MYOSTATIN.  
 OS Ictalurus punctatus (Channel catfish).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Siluriformes; Ictaluridae; Ictalurus.  
 OX NCBI\_TaxID=7998;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kocbas A.M., Liu Z.J.;  
 RT "Molecular characterization and expression of the myostatin gene from  
 channel catfish (Ictalurus punctatus).";  
 RT Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF396747; AAK84666.1; -  
 SQ SEQUENCE 389 AA; 43600 MW; 569FB952B7E9E173 CRC64;

Query Match 89.6%; Score 563; DB 13; Length 389;  
 Best Local Similarity 89.7%; Pred. No. 1.3e-59;  
 Matches 96; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

```

QY 3 GLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTLHV 62
DB 283 GLDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTLHV 342
QY 63 QANPRGSAGPCCTPTLMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 109
DB 343 KANPRGTAGPCTPTKMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 389

RESULT 9
ID Q90M05 PRELIMINARY; PRT: 385 AA.
AC Q90M05:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN.
OS Sparus aurata (gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA Maccacozzo L., Bargelloni L., Radaelli G., Mascarello F.,
RA Patarinello T.;
RT "Characterization of the myostatin gene in the gilthead seabream,
RT Sparus aurata: sequence, genomic structure, and expression pattern.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF288448; AAK53545.1; -
DR EMBL: AF288447; AAK53544.1; -
SQ SEQUENCE 385 AA; 43704 MW; 18F902CE325A3916 CRC64;

Query Match 89.2%; Score 560; DB 13; Length 385;
Best Local Similarity 89.0%; Pred. No. 3e-59;
Matches 97; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DFLGDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 60
DB 277 DSGLCDENSPESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 336
QY 61 VQANPRGSAGPCCTPTLMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 109
DB 337 VKNANPRGSAGPCCTPTKMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 385

RESULT 10
ID Q9DD18 PRELIMINARY; PRT: 373 AA.
AC Q9DD18:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN PRECURSOR.
OS Gdf-8.
OC Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Andersen O.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]

```

```

RP SEQUENCE FROM N.A.
RA Ostbye T.K., Galloway T.F., Nielsen C., Gabestad I., Bardal T.,
RA Andersen O.;
RT "The two myostatin genes of Atlantic salmon (Salmo salar) are
RT expressed in a variety of tissues.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AJ297267; CAC19541.2; -
DR EMBL: AJ316006; CAC59700.1; -
DR HSSP: P12643; 3BMP.
DR InterPro: IPR001839; TGF-beta.
DR InterPro: IPR001111; TGFb_M.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 265 373 MYOSTATIN.
SQ SEQUENCE 373 AA; 41896 MW; C641D71D83E66C4D CRC64;

Query Match 88.7%; Score 557; DB 13; Length 373;
Best Local Similarity 88.1%; Pred. No. 6.7e-59;
Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DFLGDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 60
DB 265 DSGLCDENSPESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 324
QY 61 VQANPRGSAGPCCTPTLMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 109
DB 325 VKNANPRGTAGPCTPTKMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 373

RESULT 11
ID Q90ZD2 PRELIMINARY; PRT: 373 AA.
AC Q90ZD2:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSTATIN 1.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Rescan P.-Y., Jutel I., Ralliere C.;
RT "Two myostatin genes are differentially expressed in myotomal muscle
RT of the trout (Oncorhynchus mykiss).";
RL J. Exp. Biol. 0:0-0(2001).
DR EMBL: AF273035; AAK71707.1; -
SQ SEQUENCE 373 AA; 42049 MW; 9DD4771B5CF671EA CRC64;

Query Match 88.7%; Score 557; DB 13; Length 373;
Best Local Similarity 88.1%; Pred. No. 6.7e-59;
Matches 96; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DFLGDCDEHSTESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 60
DB 265 DSGLCDENSPESRCRRPLTVDFEAFGMDWIIAPKRRKANYCSGCECFVFLQKYPHTL 324
QY 61 VQANPRGSAGPCCTPTLMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 109
DB 325 VKNANPRGTAGPCTPTKMSPTNMLYFNKKEQIITYGKIPAMVYDRCGS 373

RESULT 12
ID Q90ZD1 PRELIMINARY; PRT: 373 AA.
AC Q90ZD1:

```







GenCore version 4.5  
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OW protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 16.7 Seconds  
(without alignments)  
627.170 Million cell updates/sec

Title: US-09-754-826-2  
Perfect score: 628  
Sequence: 1 DFGDCDEHSTESRCRYPL.....KEQIIVGKIPAMVVDRCGCS 109

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	39.3	370	2	I51199
2	241	38.4	255	2	I48235
3	241	38.4	411	2	B41398
4	237.5	37.8	115	2	PN0506
5	235	37.4	349	1	WFP058
6	235	37.4	407	1	A40150
7	235	37.4	408	2	S50899
8	234.5	37.3	393	2	I50103
9	232.5	37.0	115	2	PN0505
10	225.5	35.9	207	2	S37618
11	225.5	35.9	513	1	BMH06
12	223.5	35.6	510	2	A54798
13	212.5	33.8	313	2	I51284
14	212.5	33.8	360	2	A29619
15	211.5	33.7	125	2	S43295
16	211.5	33.7	352	2	JC5366
17	211.5	33.7	352	2	S70580
18	211.5	33.7	436	2	B55452
19	211	33.6	373	2	PM0042
20	210.5	33.5	413	2	JC4862
21	210.5	33.5	424	1	WFP058
22	210.5	33.5	424	1	S31440
23	210.5	33.5	424	1	B40905
24	210.5	33.5	425	1	S50898
25	210.5	33.5	425	2	I47072
26	210.5	33.5	426	1	B24248
27	210.5	33.5	426	2	JH0690
28	209.5	33.4	367	2	JC4151
29	209.5	33.4	431	1	BMH07

30	208.5	33.2	352	2	JC2466	inhibin beta-C cha
31	207.5	33.0	151	2	S43296	bone morphogenetic
32	207.5	33.0	430	2	J01184	osteogenic protein
33	206.5	32.9	495	2	S43294	bone morphogenetic
34	206.5	32.9	501	2	A53452	cartilage-derived
35	206.5	32.9	501	2	JC2347	growth/differentia
36	205.5	32.7	402	2	A45056	osteogenic protein
37	204.5	32.6	350	2	JC5241	activin beta E cha
38	204	32.5	350	2	T25451	transforming growt
39	204	32.5	393	2	S37073	bone morphogenetic
40	204	32.5	394	2	S45355	bone morphogenetic
41	204	32.5	396	1	BMH02	bone morphogenetic
42	204	32.5	398	2	JH0688	bone morphogenetic
43	204	32.5	398	2	JH0687	bone morphogenetic
44	203	32.3	353	2	I50607	bone morphogenetic
45	201.5	32.1	409	2	S01825	transforming growt

## ALIGNMENTS

RESULT 1  
I51199  
activin beta B subunit - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I51199  
R:Dohmann, C.E.; Hemmati-Briyvanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt  
Dev. Biol. 157, 474-483, 1993  
A>Title: Expression of activin mRNA during early development in Xenopus laevis.  
A:Reference number: I51199; MUID:93273083  
A:Accession: I51199  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-370 <DOH>  
A:Cross-references: GB:S61773; NID:q386027; PIDN:AAB26863.1; PID:q386028  
C:Superfamily: inhibin

Query Match 39.3%; Score 247; DB 2; Length 370;  
Best Local Similarity 41.5%; Pred. No. 3.1e-19;  
Matches 49; Conservative 17; Mismatches 38; Indels 14; Gaps 5;

OY 3 GLDCDEHSTESRCRYPLVDFEAFGW-DWIIAPKRYKANGSGCEPFLQKYP----- 56  
Db 256 GLDCDGHF--NLCCRQFYIDFRLIGNMDIILAPAGYGVKCGSCF-ATLAVPGSASS 312  
OY 57 -HTHLVHQANPR---GSAGPCCTPTLMSPIINMLYFNGKEQIIVGKIPAMVVDRCGCS 109  
Db 313 FHTAVVAVQYRMRCGLNPQTVNSCCIPKLTSTMSMLYFDEYNIYKRDVPMNIVDECGCA 370

RESULT 2  
I48235  
inhibin beta-B chain - mouse (fragment)  
N:Alternate names: activin bB chain  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 01-Aug-1997 #text\_change 16-Jul-1999  
C:Accession: I48235; I48266; S31441  
R:Rlyovs, O.; Tuurti, T.; Eramaa, M.; Salnio, K.; Hilden, K.; Saxen, L.; Gilbert, S.F.  
Mech. Dev. 50, 229-245, 1995  
A>Title: Activin disrupts epithelial branching morphogenesis in developing glandular  
A:Reference number: I48235; MUID:95344997  
A:Accession: I48235  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-234 <RES>  
A:Cross-references: EMBL:X83376; NID:g603571; PIDN:CAA58290.1; PID:g603572  
R:Albanio, R.M.; Groome, N.; Smith, J.C.  
Development 117, 711-723, 1993  
A>Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cel  
A:Reference number: I48243; MUID:93321614  
A:Accession: I48266



```

A::Title: Activin B: precursor sequences, genomic structure and in vitro activities.
A::Reference number: A40150; MUID:90114200
A::Accession: A40150
A::Molecule type: DNA
A::Residues: 1-407 <MAS>
A::Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827
R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A::Title: Structure of two human ovarian inhibins.
A::Reference number: A90123; MUID:86186863
A::Accession: C24248
A::Molecule type: mRNA
A::Residues: 55-407 <MA2>
A::Cross-references: GB:M13437; NID:g186416; PIDN:AAA59169.1; PID:g186417
R:Feng, Z.M.; Baird, C.W.; Chen, C.L.C.
Mol. Endocrinol. 3, 939-948, 1989
A::Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.
A::Reference number: A40156; MUID:89295443
A::Accession: A40156
A::Molecule type: mRNA
A::Residues: 22-46, 'A', 48-407 <EN>
A::Cross-references: GB:M31632
A::Experimental source: testis
R:Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.
Biochim. Biophys. Acta 1039, 135-141, 1990
A::Title: Purification and characterization of recombinant human activin B.
A::Reference number: S10751; MUID:90304183
A::Accession: S10751
A::Molecule type: protein
A::Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>
C::Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.
A::Gene: GDB:INHBB
A::Cross-references: GDB:I19347; OMIM:147390
A::Map position: 2cen-2q13
C::Superfamily: Inhibin
C::Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-292/Domain: propeptide #status predicted <PRO>
F:293/Product: inhibin beta-B chain #status predicted <MAV>
F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          37.4%; Score 235; DB 1; Length 407;
Best Local Similarity 39.8%; Pred. No. 7e-18;
Matches 47; Conservative 18; Mismatches 39; Indels 14; Gaps 5;

OY      3 GLDCDEHSTESKCCRPILTVDFEAFGW-DWIIAPKKRYANICSGCECFVLQKP----- 56
        ||::| : : |::| : |::| | | | | | | | | | | | | | | | | | | | | |
Db      293 GLECGGRT--MLCCROQGFIFRLTIGWMWDIAPGYGVGCSCSP--AYLAGVGSASS 349

OY      57 -HTHVHOANPR----GSAGPCCTPLMSPIINMLTFENKEQIIYKIPAMVVDRCGS 109
        ||::| : |::| : |::| | | | | | | | | | | | | | | | | | | | | |
Db      350 FHTAVVNOIRMGGLNPGRIVNSCCIPTKLSTMSLTFDEYNIVKRQVPMIVBEGCA 407

RESULT      7
S50899
betab inhibin precursor - bovine
C::Species: Bos primigenius taurus (cattle)
C::Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C::Accession: S50899
R:Thompson, D.A.; Cronin, C.N.; Martin, F.
Eur. J. Biochem. 226, 751-764, 1994
A::Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and beta(B) DNase I footprinting.
A::Reference number: S50897; MUID:95112839
A::Accession: S50899
A::Status: preliminary
A::Molecule type: DNA
A::Residues: 1-408 <THO>
A::Cross-references: EMBL:U16240

```

C:Genetics: 1  
A:introns: 151/1  
C:Superfamily: Inhibin

Query Match                37.4%; Score 235; DB 2; Length 408;  
Best Local Similarity     39.8%; Pred. No. 7e-18;  
Matches      47; Conservative    18; Mismatches    39; Indels    14; Gaps    5;

OY          3 GLDCEHSTESRCRYPLTVDFEAFGW-DWIIAPRRKANYCSGECSEVFLQKP----- 56  
          ||::| : || | ::|| | | | | | | | | | | |  
DB          294 GLECGGRF--NLCCKQGFFIDRLIGWMWDWIIPAGIYGVCSCGP-AVLAVGSASS    350  
  
OY          57 -HTHLVHOANPR---GSNGPCCPTLMSPIMLTFENGKEOIYYIKIRPMVVDRGCSS    109  
          ||::| : | : || | | | | | | | | | | |:  
DB          351 FRTAVVNORMGLNPVTGNNSCIPTKLSTSMELFYDEENIVKRDPVMIVEEGCA    408  
  
RESULT      8  
150103  
activin beta B - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C:date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: I50103  
R.Wittbrodt, J.: Rosa, F.M.  
Gene Dev. 8, 1448-1462, 1994  
A:title: Disruption of mesoderm and axis formation in fish by ectopic expression of a  
A:Reference number: I50103; MUID:95011555  
A:Accession: I50103  
A:status: preliminary; translated from GB/EMBL/DDBU  
A:molecule type: mRNA  
A:Residues: 1-193 <WT>  
A:CROSS-references: EMBL:X76051; NID:9516356; PIDN:CAA53636.1; PJD:9516357  
C:Genetics:  
A:gene: Zactbetab  
C:superfamily: inhibin

Query Match                37.3%; Score 234.5; DB 2; Length 393;  
Best Local Similarity     39.8%; Pred. No. 7.7e-18;  
Matches      47; Conservative    18; Mismatches    40; Indels    13; Gaps    5;

OY          3 GLDCEHSTESCRCRYPLTVDFEAFGW-DWIIAPRRKANYCSGECSEVFLQRP----- 56  
          ||::| : || | ::|| | | | | | | | | | | |:  
DB          278 GLECDSNN-GSLCCRQGFIFDLRGMDWIIAPAGIYGNCVGSCP-AYMAGVSGSASS    335  
  
OY          57 -HTHLVHOANPR---GSAGPCCTPLMSPIMLTFENGKEOIYYIKIRPMVVDRGCSS    109  
          ||::| : | : || | | | | | | | | | | |:  
DB          336 FRTAVVNORMGMSPGVNSCCIPTKLSTMSLFYDEENIVKRDPVMIVEEGCA    393  
  
RESULT      9  
PN0505  
activin beta B-1 chain - goldfish (fragment)  
N:Alternate names: gact 2  
C:Species: Carassius auratus (goldfish)  
C:date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: PN0505  
B.Che, W.; Gallin, W.J.; Strobeck, C.; Peter, R.E  
Biochem. Biophys. Res. Commun. 193, 711-717, 1993  
A:title: Cloning and sequencing of goldfish activin subunit genes: Strong structural  
A:Reference number: PN0504; MUID:93290666  
A:Accession: PN0505  
A:Molecule type: DNA  
A:Residues: 1-115 <GEW>  
C:Superfamily: inhibin

Query Match                37.0%; Score 232.5; DB 2; Length 115;  
Best Local Similarity     40.2%; Pred. No. 3.6e-18;  
Matches      47; Conservative    16; Mismatches    41; Indels    13; Gaps    5;

OY          3 GLDCDHSTESCRYPITLVDFEAFGW-DWIIAPRRKANYCSGECSEVFLQXP----- 56

Db 1 GLECD-GTGGGLCCRCQRFYIDRLIGWMDIAPAGYGNCEGSCP-AYMAGVPSCASS 58  
Oy 57 -FTHLVHQAHPNPR---GSAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVYDRCCG 108  
Db 59 FHTAVVNOYIRMGKISPGSVNSCCIPTKLSTPMWLFDEYDNIYKRDVPMNIVECCG 115

RESULT 10  
S37618  
vgr protein - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 16-Jul-1999  
C:Accession: S37618  
R:Sauremann, U.; Meyerann, R.; Schluesener, H.J.  
J. Neurosci. Res. 33, 142-147, 1992  
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning  
A:Reference number: S37618; MUID:93085758  
A:Accession: S37618  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-207 <SAU>  
C:Cross-references: EMBL:X58830; NID:957475; PIDN:CAA41634.1; PID:957476  
Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser  
C:Superfamily: Inhibin

Query Match 35.9%; Score 225.5; DB 2; Length 207;  
Best Local Similarity 41.4%; Pred. No. 3.8e-17;  
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;

Oy 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGECFVFLQKYPHTH---- 59  
Db 96 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDECSFPLNHNMTNHAIV 155  
Oy 60 --LVHQAHPNPRGSAAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVYDRCCG 108  
Db 156 QTLVHLMNPEYVPRKPCCAPTKLNAISLVLFDDNSNVILKKRYNMVYRACGC 206

RESULT 11  
BMH06  
bone morphogenetic protein 6 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 18-Oct-1991 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
C:Accession: B39263  
R:Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990  
A:Title: Identification of transforming growth factor beta family members present in bone  
A:Reference number: A39263; MUID:91088608  
A:Accession: B39263  
A:Molecule type: mRNA  
A:Residues: 1-513 <CEU>  
C:Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562  
C:Genetics:  
A:Gene: GDB:BMH6  
A:Cross-references: GDB:127596; OMIM:112266  
A:Map position: 6pter-6qter  
C:Superfamily: Inhibin  
C:Keywords: bone; glycoprotein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-374/Domain: propeptide #status predicted <PRO>  
F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>  
F:241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.9%; Score 225.5; DB 1; Length 513;  
Best Local Similarity 41.4%; Pred. No. 9.7e-17;  
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;  
Oy 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGECFVFLQKYPHTH---- 59  
Db 402 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDECSFPLNHNMTNHAIV 461

Oy 60 --LVHQAHPNPRGSAAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVYDRCCG 108  
Db 462 QTLVHLMNPEYVPRKPCCAPTKLNAISLVLFDDNSNVILKKRYNMVYRACGC 512

RESULT 12  
A54798  
Vg-1-related protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 16-Jul-1999  
C:Accession: A54798; A33925; S47442  
R:Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.  
J. Cell Biol. 126, 1595-1609, 1994  
A:Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral b  
A:Reference number: A54798; MUID:94375533  
A:Accession: A54798  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-510 <GIT>  
A:Cross-references: EMBL:X80992; NID:9530729; PIDN:CAA56917.1; PID:9530730  
R:Lyon, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan,  
Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989  
A:Title: Vgr-1, a mammalian gene related to xenopus Vg-1, is a member of the transfor  
A:Reference number: A33925; MUID:89282810  
A:Accession: A33925  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-74; 'K', 76-85, 'P', 87-510 <LYO>  
A:Cross-references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353  
C:Superfamily: Inhibin

Query Match 35.6%; Score 223.5; DB 2; Length 510;  
Best Local Similarity 41.4%; Pred. No. 1.6e-16;  
Matches 46; Conservative 13; Mismatches 45; Indels 7; Gaps 2;

Oy 5 DCDENHSTRCRCRYPLTVDFEAFGW-DWIIAPRRYKANYCGECFVFLQKYPHTH---- 59  
Db 399 DYNSELKTKACKKHELYVSFDLGMQDWIIAPRGYANAYCDECSFPLNHNMTNHAIV 458  
Oy 60 --LVHQAHPNPRGSAAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVYDRCCG 108  
Db 459 QTLVHLMNPEYVPRKPCCAPTKLNAISLVLFDDNSNVILKKRYNMVYRACGC 509

RESULT 13  
I51284  
bone morphogenetic protein-7 - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 16-Jul-1999  
C:Accession: I51284  
R:Houston, B.; Thorp, B.H.; Burt, D.W.  
J. Mol. Endocrinol. 13, 289-301, 1994  
A:Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick  
A:Reference number: I51284; MUID:9520473  
A:Accession: I51284  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-313 <HOH>  
A:Cross-references: GB:S77477; NID:g957233; PIDN:AA833846.1; PID:g957234  
C:Superfamily: Inhibin

Query Match 33.8%; Score 212.5; DB 2; Length 313;  
Best Local Similarity 40.3%; Pred. No. 1.5e-15;  
Matches 48; Conservative 14; Mismatches 44; Indels 13; Gaps 5;

Oy 2 FGID--CDENHSTSR--CCRYPLTVDFEAFGW-DWIIAPRRYKANYCGECFVFLQKYP 56  
Db 195 FGMSNIAENSSDDQKACKKHELYVSFDLGMQDWIIAPRGYANAYCDECAFP-LNSYM 253  
Oy 57 HT-----HLVHQAHPNPRGSAAGPCCPTPLMSPINMLYFNKGEOIIVGKIPAMVYDRCCG 108





GenCore version 4.5  
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OW protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 30.38 Seconds  
(Without alignments)  
398.520 Million cell updates/sec

Title: US-09-754-826-2  
Perfect score: 628  
Sequence: 1 DFGIDCDHSTESRCRYPL.....KEQIYKIPAWVDRCCGS 109

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1983.DAT:\*  
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6: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA1985.DAT:\*  
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22: /SIDSI/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	99.0	109	22	AA620141 Human growth diffe
2	622	99.0	126	15	AA63161 Mouse growth diffe
3	622	99.0	126	19	AA69883 Murine growth diffe
4	622	99.0	126	20	AA15386 C-terminal region
5	622	99.0	126	22	AA673182 Murine GDP-8 #1.
6	622	99.0	130	22	AA673189 Rat GDP-8.
7	622	99.0	160	22	AA620153 Growth differentia
8	622	99.0	226	22	AA673188 Chicken GDP-8.
9	622	99.0	254	22	AA620152 Growth differentia
10	622	99.0	362	22	AA620132 Turkey growth diffe
11	622	99.0	375	15	AA63160 Human growth diffe

12	622	99.0	375	19	AA69888 Chicken growth dif
13	622	99.0	375	19	AA69891 Pig growth diffe
14	622	99.0	375	19	AA69885 Human growth diffe
15	622	99.0	375	19	AA69885 Human growth diffe
16	622	99.0	375	20	AA63460 Human growth diffe
17	622	99.0	375	20	AA633838 Amino acid sequenc
18	622	99.0	375	20	AA633839 Amino acid sequenc
19	622	99.0	375	20	AA633840 Amino acid sequenc
20	622	99.0	375	20	AA633841 Amino acid sequenc
21	622	99.0	375	20	AA633843 Amino acid sequenc
22	622	99.0	375	20	AA633844 Amino acid sequenc
23	622	99.0	375	20	AA633937 Amino acid sequenc
24	622	99.0	375	20	AA633938 Amino acid sequenc
25	622	99.0	375	20	AA633932 Amino acid sequenc
26	622	99.0	375	20	AA633935 Amino acid sequenc
27	622	99.0	375	20	AA633935 Amino acid sequenc
28	622	99.0	375	20	AA633932 Amino acid sequenc
29	622	99.0	375	20	AA633937 Amino acid sequenc
30	622	99.0	375	21	AA633938 Amino acid sequenc
31	622	99.0	375	21	AA633932 Amino acid sequenc
32	622	99.0	375	21	AA633935 Amino acid sequenc
33	622	99.0	375	22	AA633937 Amino acid sequenc
34	622	99.0	375	22	AA633938 Amino acid sequenc
35	622	99.0	375	22	AA633932 Amino acid sequenc
36	622	99.0	375	22	AA633935 Amino acid sequenc
37	622	99.0	376	15	AA633159 Rat growth diffe
38	622	99.0	376	15	AA633159 Rat growth diffe
39	622	99.0	376	19	AA630689 Murine growth diffe
40	622	99.0	376	20	AA633837 Amino acid sequenc
41	622	99.0	376	20	AA633842 Amino acid sequenc
42	622	99.0	376	20	AA633930 Amino acid sequenc
43	622	99.0	376	20	AA633931 Amino acid sequenc
44	622	99.0	376	20	AA633193 Rat GDP-8 protein.
45	622	99.0	376	20	AA633188 Murine GDP-8 prote

## ALIGNMENTS

RESULT 1	
AA620141	standard; Protein; 109 AA.
XX	
AC	AA620141:
XX	
DT	30-APR-2001 (first entry)
XX	
DE	Human growth differentiation factor 8 C-terminal region.
XX	
KW	Growth differentiation factor 8; GDP-8; myostatin; down-regulation;
KM	vaccine; muscle; meat; cachexia; cardiant; human; mutant; muten.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200105820-A2.
XX	
PD	25-JAN-2001.
XX	
PE	20-JUL-2000; 2000WO-DK00413.
XX	
PR	20-JUL-1999; 99DK-0001014.
XX	
PR	26-JUL-1999; 99US-0145275.
XX	
PA	(MEBI-) M & E BIOTECH AS.
XX	
PI	Halkier T, Moutlsen S, Klynsner S;
XX	
DR	WPI; 2001-112680/12.
XX	
PT	Increasing the muscle mass of animals used in meat production by down
PT	regulating growth differentiation factor 8 (GDP-8) activity in the
PT	animal through induction of anti-GDP-8 antibody production

xx Claim 17; Page 93-94; 110pp; English.  
 CC The present sequence comprises the 109 amino acid residue  
 CC C-terminal region of human growth differentiation factor 8  
 CC (GDF-8), i.e. residues 267-375 of the full-length protein (see  
 CC AAB0131). The homodimer of this region is thought to be the  
 CC biologically active form of GDF-8. It is an object of the  
 CC invention to produce a recombinant therapeutic vaccine capable of  
 CC effecting down-regulation of GDF-8 in order to increase the muscle  
 CC growth rate of farm animals. Variants of GDF-8 (see AAB0145-53)  
 CC are provided that are capable of breaking autotolerance against  
 CC autologous GDF-8. These comprise the C-terminal portion of human  
 CC GDF-8 in which a portion of the native sequence is replaced by a  
 CC T-cell epitope such as the promiscuous tetanus toxin T-cell epitope  
 CC P2 or P30. The high number (9) of Cys residues in the C-terminal  
 CC region limits the possible sites in which the T-cell epitope can be  
 CC positioned without major disturbance of the native 3-dimensional  
 CC structure of the protein. Nucleic acids encoding the GDF-8 variants  
 CC can be used for genetic immunisation of the animals. Down-regulation  
 CC of GDF-8 activity can increase muscle mass by up to at least 45% in  
 CC cattle, pigs and poultry used for meat production, reducing the need  
 CC for antibiotic feed-additives. Anti-GDF8 vaccines can be used to  
 CC treat human diseases such as cancer cachexia where muscle atrophy is  
 CC pronounced and for patients suffering from acute and chronic heart  
 CC failure.

CC Sequence 109 AA:

Query Match 99.0%; Score 622; DB 22; Length 109;  
 Best Local Similarity 99.1%; Pred. No. 1.3e-59;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDDEHSTSRRCRYPLTVDFEAFGMDWIAPRKRYKANCSCGEFVFLQKYPHTL 60  
 Db 1 dfgldcdenhstsrccrypltdvdfefgwdwllaprkrykancscgecfvflqkyphtl 60  
 OY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNGKEQIIYGIKIPAMVVDRCGCS 109  
 Db 61 vhaqnprrgsagpcctptlmsptnmlfyngkeqiiygkikipamvvdrcgcs 109

RESULT 2

AAR63161 AAR63161 standard; Protein; 126 AA.

AC AAR63161;

DT 23-JUN-1995 (first entry)

Mouse growth differentiation factor-8 partial sequence.

KW Growth differentiation factor-8; GDF-8; cell proliferation;  
 KM adipocyte; obesity; transforming growth factor-beta.

OS Mus musculus.

PN W09421681-A.

PD 29-SEP-1994.

PF 18-MAR-1994; 94WO-US03019.

PR 19-MAR-1993; 93US-0033923.

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.

PI Lee S, McPherron AC;

DR WPI; 1994-437444/39.

DR Q-PSDB; Q76380.

XX

PT New growth differentiation factor 8 - useful for treatment and  
 PT diagnosis of cell proliferative disorders esp. of muscle.  
 XX  
 PS Disclosure; Page 41; 84pp; English.  
 CC GDF-8 can be used to maintain cells before transplantation; to  
 CC improve efficiency of cell fusion and to treat obesity or diseases  
 CC related to abnormal adipocyte proliferation.  
 XX  
 SQ Sequence 126 AA:

Query Match 99.0%; Score 622; DB 15; Length 126;  
 Best Local Similarity 99.1%; Pred. No. 1.6e-59;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DGLDDEHSTSRRCRYPLTVDFEAFGMDWIAPRKRYKANCSCGEFVFLQKYPHTL 60  
 Db 1 dfgldcdenhstsrccrypltdvdfefgwdwllaprkrykancscgecfvflqkyphtl 77  
 OY 61 VHQANPRGSAGPCCTPTLMSPTNMLYFNGKEQIIYGIKIPAMVVDRCGCS 109  
 Db 78 vhaqnprrgsagpcctptlmsptnmlfyngkeqiiygkikipamvvdrcgcs 126

RESULT 3

AAM69883 AAM69883 standard; Protein; 126 AA.

AC AAM69883;

DT 07-DEC-1998 (first entry)

DE Murine growth differentiation factor-8 C-terminal fragment.

KW Growth differentiation factor-8; GDF-8; mouse; transgenic animal;  
 KM transforming growth factor-beta; muscle; meat; inhibitor; obesity;  
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;  
 therapy.

OS Mus sp.

PN W09833887-A1.

PD 06-AUG-1998.

PF 05-FEB-1998; 98WO-US02479.

PR 23-MAY-1997; 97US-0862445.

PR 05-FEB-1997; 97US-0795071.

PR 28-APR-1997; 97US-0847910.

PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PI Lee S, McPherron AC;

DR WPI; 1998-437444/37.

DR N-PSDB; AAV45809.

XX

XX

XX

XX

XX

XX

Transgenic animals with gene for growth differentiation factor-8  
 disrupted - have increased muscle and reduced cholesterol contents,  
 PT also use of GDF-8 inhibitors for treating cancer, obesity,  
 PT neuromuscular disease  
 XX  
 PS Example 2; Page 58; 125pp; English.  
 XX This is the amino acid sequence of the C-terminal portion of mouse





```

XX 19-AUG-1999; 99US-0378238.
PR (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA
XX Lee S, McPherron AC;
XX WPI: 2001-211209/21.
DR N-PSDB: AAF63547.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia
PT
PS Example 2; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), muscledenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.
CC
XX Sequence 126 AA:
SO
Query Match 99.0%; Score 622; DB 22; Length 126;
Best Local Similarity 99.1%; Pred. No. 1.6e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLCDDEHSTESRCRRPLTVDFEAFGMDWTIAPRKRYKANSCEGEFVLQKYPHTL 60
DB 18 dfgldcdenstescrrcrrpltvdfefgwdwllapkrkyanycsgcecfvllqkyphtl 77
QY 61 VHOAMPKRSAGPCPCPTLMSPTNMLYFNKGKEQIIYKGIKIPAMVVDRCGS 109
DB 78 vhoampkrsagpcpcptlmsptnmllyfngkeqiiykgikipamvvdrcgs 126
RESULT 6
AAB73189
ID AAB73189 standard; Protein: 130 AA.
AAB73189;
DT 11-MAY-2001 (first entry)
XX
DE Rat GDF-8.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; muscledenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease.
XX
OS Rattus sp.
XX
PN WO200112777-A2.
XX
PJ 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22884.
XX
PR 19-AUG-1999; 99US-0378238.
XX

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PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;
XX WPI: 2001-211209/21.
DR N-PSDB: AAF63535.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia
PT
PS Example 9; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a GDF-8 protein,
CC which was isolated in the present invention. GDF-8 is useful for treating
CC neurodegenerative diseases (e.g. amyotrophic lateral sclerosis and
CC muscular dystrophy), muscledenerative diseases or in tissue repair due
CC to trauma, obesity and disorders related to abnormal proliferation of
CC adipocytes. GDF-8 is also useful for treating malignancies of the various
CC organ systems, particularly cells in muscle or adipose tissues and in
CC gene therapy for the treatment of cell proliferative or immunological
CC diseases mediated by GDF-8. In addition, GDF-8 is also useful for
CC treating muscle wasting disease, neuromuscular disorder, spinal cord
CC injury, traumatic injury, congestive obstructive pulmonary disease
CC (COPD), AIDS or cachexia.
CC
XX Sequence 130 AA:
SO
Query Match 99.0%; Score 622; DB 22; Length 130;
Best Local Similarity 99.1%; Pred. No. 1.6e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFGLCDDEHSTESRCRRPLTVDFEAFGMDWTIAPRKRYKANSCEGEFVLQKYPHTL 60
DB 22 dfgldcdenstescrrcrrpltvdfefgwdwllapkrkyanycsgcecfvllqkyphtl 81
QY 61 VHOAMPKRSAGPCPCPTLMSPTNMLYFNKGKEQIIYKGIKIPAMVVDRCGS 109
DB 82 vhoampkrsagpcpcptlmsptnmllyfngkeqiiykgikipamvvdrcgs 130
RESULT 7
AAB20153
ID AAB20153 standard; Protein: 160 AA.
AAB20153;
DT 30-APR-2001 (first entry)
XX
DE Growth differentiation factor 8 AutoVac construct GDF-8 ext.
XX
KW Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW cardiant; human; mutant; mutain.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Clostridium tetani.
OS Synthetic.
XX
XX Key
XX FH Location/Qualifiers
XX FT 1..15
XX FT /note= "identical to residues 215-230 of human
XX FT GDF-8"
XX
FT Region
FT 16..36
FT /note= "tetanus toxoid p30 epitope"
FT Region
FT 37..51
FT /note= "tetanus toxoid p2 epitope"
FT Region
FT 52..160
FT /note= "identical to residues 267-375 of human
FT GDF-8"
FT

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KM T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW cardiant; human; mutant; mutein.
XX Chimeric - Homo sapiens.
OS Chimeric - Clostridium tetani.
OS Synthetic.
XX Key
FH Location/Qualifiers
FT Region 1..109
   /note= "109 C-terminal residues of human GDF-8"
FT Region 110..124
   /note= "tetranus toxoid P2 epitope"
FT Region 125..145
   /note= "tetranus toxoid P30 epitope"
FT Region 146..254
   /note= "109 C-terminal residues of human GDF-8"
FT MISC-difference 90..91
   /note= "optionally replaced by Glu-Gly"
FT MISC-difference 235..236
   /note= "optionally replaced by Glu-gly"
PN WO200105820-A2.
PN 25-JAN-2001.
PX 20-JUL-2000; 2000WO-DK00413.
PX 20-JUL-1999; 99DK-0001014.
XX 26-JUL-1999; 99US-0145275.
PA (MEBI-) M & E BIOTECH AS.
PI Halkier T, Mouritsen S, Klysner S;
DR WPI; 2001-112680/12.
XX Increasing the muscle mass of animals used in meat production by down
PT regulating growth differentiation factor 8 (GDF-8) activity in the
PT animal through induction of anti-GDF-8 antibody production -
XX Example 1; Page 105-106; 110pp; English.
CC The present sequence is that of Autovac construct GDF-8 dimer
CC comprising 2 copies of the 109-amino acid C-terminal region of human
CC growth differentiation factor 8 (GDF-8, see AAF20141) covalently
CC connected through the P2 and P30 T-cell epitopes (see AAB20143-44)
CC of tetanus toxin. It is an object of the invention to produce a
CC recombinant therapeutic vaccine that is capable of effecting
CC down-regulation of GDF-8 in order to increase the muscle growth
CC rate of farm animals. The vaccines (see AAB20145-53) are capable
CC of breaking autotolerance against autologous GDF-8. They comprise
CC the C-terminal portion of human GDF-8 in which a portion of the
CC native sequence is replaced by a T-cell epitope such as P30, with
CC minimal disturbance of the authentic 3-dimensional structure of
CC the protein. Nucleic acids encoding the GDF-8 variants can be used
CC for genetic immunisation of the animals. Down-regulation of GDF-8
CC activity can increase muscle mass by up to at least 45% in cattle,
CC pigs and poultry used for meat production, reducing the need for
CC antibiotic feed-additives. Anti-GDF8 vaccines can be used to
CC treat human diseases such as cancer cachexia where muscle atrophy is
CC pronounced and for patients suffering from acute and chronic heart
CC failure.
XX Sequence . 254 AA;
SO
Query Match 99.0%, Score 622; DB 22; Length 254;
Best Local Similarity 99.1%; Pred. No. 3.3e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps
1 DFGDGDHSHNESRCCRRLPLVYDFEAFQMDWITIAKKRYKANCSGECEVFLOKKYPHNHL 60
1 dfgdgdshshnesrcrrlplvydfefqmdwtiaakrykancsgecevflokkypnhnl 60

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0Y      61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOITIGKIPAMVVDRCGS 109
        ||||||||||||||| ||||||||||||||||||||||||||||||||
Db      61 vhgandprgsagpcctptlmsptnmllyfngkeqil1y9k1pamvvdrcgs 109

RESULT 10
ID      AAB20132
AC      AAB20132 standard; Protein: 362 AA.
AS      AAB20132;
DT      30-APR-2001 (first entry)
DE      Turkey growth differentiation factor 8.
KW      Growth differentiation factor 8; GDF-8; myostatin; down-regulation;
        vaccine; muscle; meat; cachexia; cardiatic; turkey.
OS      Meleagris gallopavo.
PN      WO200105820-A2.
PD      25-JAN-2001.
PR      20-JUL-2000; 2000WO-DK00413.
PR      20-JUL-1999; 99DK-0001014.
PR      26-JUL-1999; 99US-0145225.
PA      (MEBI-) M & E BIOTECH AS.
PI      Halkier T, Mouritsen S, Klysnar S;
PI      WPI: 2001-112680/12.
PT      Increasing the muscle mass of animals used in meat production by down
        regulating growth differentiation factor 8 (GDF-8) activity in the
        animal through induction of anti-GDF-8 antibody production
        Example 1; Page 76-78; 110pp; English.

XX      The present sequence is that of turkey growth differentiation factor
XX      8 (GDF-8), also called myostatin. It is an object of the invention
XX      to produce a recombinant therapeutic vaccine capable of effecting
XX      down-regulation of GDF-8 in order to increase the muscle growth
XX      rate of farm animals. Variants of GDF-8 (see AAB20145-53) are
XX      provided that are capable of breaking autotolerance against
XX      autologous GDF-8. These comprise a C-terminal portion of human
XX      GDF-8 in which a portion of the native sequence is replaced by a
XX      T-cell epitope such as the promiscuous tetanus toxin T-cell epitope
XX      P2 or P30. Nucleic acids encoding the GDF-8 variants can be used
XX      for genetic immunisation of the animals. Down-regulation of GDF-8
XX      activity is used to increase muscle mass by up to at least 45%
XX      in cattle, pigs and poultry used for meat production, reducing the
XX      need for antibiotic feed-additives. Anti-GDF8 vaccines can be used
XX      to treat human diseases such as cancer cachexia where muscle atrophy
XX      is pronounced and for patients suffering from acute and chronic
XX      heart failure.
XX
SO      Sequence 362 AA;

Query Match 99.0%; Score 622; DB 22; Length 362;
Best Local Similarity 99.1%; Pred. No. 4.9e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

0Y      1 DFGIDCDEHSTESRCRCRYPLTVDFEAFGDMWIIARRYKANYCSGCECFVFLQKYPTHTL 60
        |||||||
Db      254 dfgidcdenhstesrcrcrypltvdfefagdmwiiarkrykanycsgecfvflqkyphthl 313
        |||||||
0Y      61 VHQANPRGSAGPCCTPTLMSPTNMLYFNKGEOITIGKIPAMVVDRCGS 109
        ||||||||||||||| ||||||||||||||||||||||||||||||||

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Db 314 vhgagprgsagpccptkmsplnmlyfngkeqilygkkipamvvdrcgs 362

RESULT 11
AA63160
ID AA63160 standard; Protein; 375 AA.
AC AAR63160;
XX
XX 23-JUN-1995 (first entry)
DE
XX Human growth differentiation factor-8 protein.
XX
XX Growth differentiation factor-8; GDF-8; cell proliferation;
KW adipocyte; obesity; transforming growth factor-beta.
XX
XX Homo sapiens.
XX
XX WO9421681-A.
XX
XX 29-SEP-1994.
XX
XX 18-MAR-1994; 94WO-US03019.
XX
XX 19-MAR-1993; 93US-0033923.
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.
XX
XX Lee S, McPherron AC;
XX
XX WPI: 1994-316943/39.
XX
XX Q-PSDB: Q76372.
XX
XX New growth differentiation factor 8 - useful for treatment and
XX diagnosis of cell proliferative disorders esp. of muscle.
XX
XX Claim 3; Page 58; 84pp: English.
XX
XX GDF-8 can be used to maintain cells before transplantation; to
XX improve efficiency of cell fusion and to treat obesity or diseases
XX related to abnormal adipocyte proliferation.
XX
XX Sequence 375 AA;

Query Match 99.0%; Score 622; DB 15; Length 375;
Best Local Similarity 99.1%; Pred. No. 5,1e-59;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0,

OY 1 DPGLCDHSHRESRCRCRPLTVDFEAFGDMWIIARRRKANKCSEGCSEVFLOKYPHTL 60
Db 267 dfgldcdeshstescrcrypltdfaigwdaiapkrykanycsgecsevfllqkyphtl 326
OY 61 VHOANPRGSAGPCCTPLTMSPINMLYFNGKEQIIYGIKIPAMVVDRCGS 109
Db 327 vhgagprgsagpccptkmsplnmlyfngkeqilygkkipamvvdrcgs 375

RESULT 12
AA69888
ID AA69888 standard; Protein; 375 AA.
AC AAW69888;
XX
XX 07-DEC-1998 (first entry)
DE
XX Chicken growth differentiation factor-8.
XX
XX Growth differentiation factor-8; GDF-8; chicken; transgenic animal;
KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;
XX therapy.
XX

```

OS	Gallus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Cleavage-site	263...266
FT	Protein	267...375
XX		/Label= Mat_protein
PX	MO9833867-AI.	
XX		
PD	06-AUG-1998.	
XX		
PF	05-FEB-1998;	98WO-US02479.
XX		
PR	23-MAY-1997;	97US-0862445.
PR	05-FEB-1997;	97US-0795071.
PR	28-APR-1997;	97US-0847910.
XX		
PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.	
PI	Lee S, McPherron AC:	
DR	WPI; 1998-437444/37.	
DR	N-PSDB; AAV45819.	
XX		
PT	Transgenic animals with gene for growth differentiation factor-8	
PT	disrupted - have increased muscle and reduced cholesterol contents,	
PT	also use of GDF-8 inhibitors for treating cancer, obesity,	
PT	neuromuscular disease	
XX		
PS	Example 9; Fig 14c; 125pp; English.	
XX		
CC	This is the amino acid sequence of chicken growth differentiation	
CC	factor-8 ( <del>GDF-8</del> ). <del>a novel member of the transforming growth factor-</del>	
CC	beta superfamily that appears to relate to various cell	
CC	proliferative disorders, especially those involving muscle, nerve	
CC	and adipose tissue. The sequence was deduced from a cDNA clone	
CC	(see AAV45819) isolated from a skeletal muscle CDNA library. The	
CC	invention provides novel mammalian and avian GDF-8 proteins (see	
CC	AAM9883-92). A transgenic non-human animal is claimed in which	
CC	GDF-8 expression is disrupted or interfered with. Also claimed	
CC	are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb	
CC	from these animals; (2) method for increasing muscle mass in	
CC	animals by administering an antibody (Ab) that binds to GDF-8; (3)	
CC	inhibiting the action of GDF-8 by treating foetal or adult muscle	
CC	or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic	
CC	acid encoding a GDF-8 protein truncated by loss of the C-terminal	
CC	active fragment. The transgenic animals have increased muscle mass	
CC	and for poultry reduced cholesterol contents. Method (3) is used	
CC	to treat muscle wasting or neuromuscular diseases, muscular atrophy	
CC	and aging, particularly muscular dystrophy, spinal cord or	
CC	traumatic injuries, congestive or obstructive lung disease, AIDS	
CC	and cachexia. Method (4) is used to treat cancer of muscle,	
CC	connective tissue and bone, or obesity. Also (not claimed) GDF-8	
CC	can be used to maintain myoblasts intended for transplanting or to	
CC	improve efficiency of fusion. Ab can be used to detect and	
CC	quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),	
CC	also for immunotherapy and in vivo imaging.	
XX		
SQ	Sequence 375 AA:	
	Query Match 99.0%; Score 622; DB 19; Length 375;	
	Best Local Similarity 99.1%; Pred. No. 5, le-59;	
	Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 DFGDDCDEHSTSRCCRPLVVDPEAFGMDWIIPAKRYAANTCSGCBEFVLQKYPHRL 60 	
Db	267 dfgldcdeshstsrccrpyltvdfeafgwdwiapkrxykanycsgecefvllqkyphthl 326 	
OY	61 VHQANPDSAGPCCPITLMSPTINMLYFNKKEQIIYIGKIPAMVVDRGGC 109 	
Db	327 vhnqanprdsagpcclptkmisplmlyfngkeqillygklpamvvdrrggc 375 	

RESULT 13  
 AAM69891  
 ID AAM69891 standard; Protein; 375 AA.  
 AC AAM69891;  
 DT 07-DEC-1998 (first entry)  
 XX  
 DE Pig growth differentiation factor-8.  
 XX  
 KW Growth differentiation factor-8; GDF-8; pig; transgenic animal;  
 KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;  
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;  
 KW therapy.  
 XX  
 OS Sus scrofa.  
 XX  
 FH Key Location/Qualifiers  
 FT Cleavage-site 263..266  
 FT Protein 267..375  
 FT /label= Mat\_protein  
 XX  
 MO9833887-A1.  
 PD 06-AUG-1998.  
 XX  
 PF 05-FEB-1998; 98WO-US02479.  
 XX  
 PR 23-MAY-1997; 97US-0862445.  
 PR 05-FEB-1997; 97US-0795071.  
 PR 28-APR-1997; 97US-0847910.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 PI Lee S, McPherron AC;  
 XX  
 DR WPI: 1998-437444/37.  
 DR N-PSDB: AAV45822.  
 XX  
 PT Transgenic animals with gene for growth differentiation factor-8  
 PT disrupted - have increased muscle and reduced cholesterol contents,  
 PT also use of GDF-8 inhibitors for treating cancer, obesity,  
 PT neuromuscular disease  
 XX  
 PS Example 9; Fig 14f; 125pp; English.  
 CC This is the amino acid sequence of porcine growth differentiation  
 CC factor-8 (GDF-8), a novel member of the transforming growth factor-  
 CC beta superfamily that appears to relate to various cell  
 CC proliferative disorders, especially those involving muscle, nerve  
 CC and adipose tissue. The sequence was deduced from a cDNA clone  
 CC (see AAV45822) isolated from a skeletal muscle cDNA library. The  
 CC invention provides novel mammalian and avian GDF-8 proteins (see  
 CC AAM69883-92). A transgenic non-human animal is claimed in which  
 CC GDF-8 expression is disrupted or interfered with. Also claimed  
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb  
 CC from these animals; (2) method for increasing muscle mass in  
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)  
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle  
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic  
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal  
 CC active fragment. The transgenic animals have increased muscle mass  
 CC and for poultry reduced cholesterol contents. Method (3) is used  
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy  
 CC and aging, particularly muscular dystrophy, spinal cord or  
 CC traumatic injuries, congestive or obstructive lung disease, AIDS  
 CC and cachexia. Method (4) is used to treat cancer of muscle,  
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8  
 CC can be used to maintain myoblasts intended for transplanting or to  
 CC improve efficiency of fusion. Ab can be used to detect and  
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),  
 CC also for immunotherapy and in vivo imaging.

XX SQ Sequence 375 AA:  
 Query Match 99.0%; Score 622; DB 19; Length 375;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 DFGLCDDEHSTFESRCRCRYPLVDFEAFGMDWIIAPKRYKANYCSGECEFFLQKYPHTL 60  
 DB 267 dfgldcddehstfescrcryplvdfefgmdwiiapkrkykanycsgecefflqkyphtl 326  
 OY 61 VHQANPRGSAGPCCPPTLMSPINMLYFNKGEDITIGKIPAMVVDRCGS 109  
 DB 327 vhnqanprgsagpcctptlmspinmlyfngkeditygkipamvvdrcgcs 375  
 RESULT 14  
 AAM69885  
 ID AAM69885 standard; Protein; 375 AA.  
 AC AAM69885;  
 DT 07-DEC-1998 (first entry)  
 XX  
 DE Human growth differentiation factor-8.  
 XX  
 KW Growth differentiation factor-8; GDF-8; human; transgenic animal;  
 KW transforming growth factor-beta; muscle; meat; inhibitor; obesity;  
 KW neuromuscular disease; muscular dystrophy; cachexia; AIDS; cancer;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 71..73  
 FT /note= "Asn is N-glycosylated"  
 FT Cleavage-site 263..266  
 FT Protein 267..375  
 FT /label= Mat\_protein  
 XX  
 PN MO9833887-A1.  
 PD 06-AUG-1998.  
 XX  
 PF 05-FEB-1998; 98WO-US02479.  
 XX  
 PR 23-MAY-1997; 97US-0862445.  
 PR 05-FEB-1997; 97US-0795071.  
 PR 28-APR-1997; 97US-0847910.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 PI Lee S, McPherron AC;  
 XX  
 DR WPI: 1998-437444/37.  
 DR N-PSDB: AAV45813.  
 XX  
 PT Transgenic animals with gene for growth differentiation factor-8  
 PT disrupted - have increased muscle and reduced cholesterol contents,  
 PT also use of GDF-8 inhibitors for treating cancer, obesity,  
 PT neuromuscular disease  
 XX  
 PS Example 3; Fig 5c; 125pp; English.  
 CC This is the amino acid sequence of human growth differentiation  
 CC factor-8 (GDF-8), a novel member of the transforming growth factor-  
 CC beta superfamily that appears to relate to various cell  
 CC proliferative disorders, especially those involving muscle, nerve  
 CC and adipose tissue. The sequence was deduced from a cDNA clone  
 CC (see AAV45810) isolated from a skeletal muscle cDNA library. The  
 CC invention provides novel mammalian and avian GDF-8 proteins (see  
 CC AAM69883-92). A transgenic non-human animal is claimed in which

CC GDF-8 expression is disrupted or interfered with. Also claimed  
 CC are: (1) chicken or turkey eggs or meat, beef, milk, pork and lamb  
 CC from these animals; (2) method for increasing muscle mass in  
 CC animals by administering an antibody (Ab) that binds to GDF-8; (3)  
 CC inhibiting the action of GDF-8 by treating foetal or adult muscle  
 CC or progenitor cells with a GDF-8 inhibitor; (4) isolated nucleic  
 CC acid encoding a GDF-8 protein truncated by loss of the C-terminal  
 CC active fragment. The transgenic animals have increased muscle mass  
 CC and for poultry reduced cholesterol contents. Method (3) is used  
 CC to treat muscle wasting or neuromuscular diseases, muscular atrophy  
 CC and aging, particularly muscular dystrophy, spinal cord or  
 CC traumatic injuries, congestive or obstructive lung disease, AIDS  
 CC and cachexia. Method (4) is used to treat cancer of muscle,  
 CC connective tissue and bone, or obesity. Also (not claimed) GDF-8  
 CC can be used to maintain myoblasts intended for transplanting or to  
 CC improve efficiency of fusion. Ab can be used to detect and  
 CC quantify GDF-8 (particularly in muscle, for diagnosis or monitoring),  
 CC also for immunotherapy and in vivo imaging.

Sequence 375 AA:

Query Match 99.0%; Score 622; DB 19; Length 375;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTESRCRRYPLTVDFEAFGMDWIAPRKRYKANVCSGCEPFVLOKYPHTL 60  
 Db 267 dfgldcdenstescrrcrrypltvdfefgwdwliaprrykanvcsgecefvlqkyphtl 326  
 OY 61 VHOANPRGSAGPCCPTPLMSPIMLYFNKGKQIITYGKIPAMVVDRCGCS 109  
 Db 327 vhoanprgsagpccptplmspimlmyfnkgkqilygkipamvvdrcgcs 375

RESULT 15

AAW65460  
 ID AAW65460 standard; Protein; 375 AA.

AC AAW65460;

DT 09-NOV-1998 (first entry)

DE Human growth differentiation factor-8.

DE Growth differentiation factor-8; GDF-8; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 71 /note="N-glycosylated"

FT Cleavage-site 263..266 /note="RXXR proteolytic cleavage site"

XX WO9835019-A1.

XX 13-AUG-1998.

XX 06-FEB-1998; 98WO-US02310.

XX 06-FEB-1997; 97US-0795671.

XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Lee S, McPherron AC, v

XX WPI; 1998-447217/38.

XX Transgenic animal growth differentiation factor-11 is inhibited - by  
 PT insertion of transgene, also use of GDF-11 inhibitors for treating  
 PT muscular wasting, neuromuscular disease, obesity

PS Example 3; Page 55-56; 89pp; English.

XX This is the amino acid sequence of human growth differentiation  
 CC factor-8 (GDF-8). It shows a high degree of sequence homology  
 CC to the newly identified human growth differentiation factor-11  
 CC (GDF-11, see AAW65458). Alignment of the GDF-8 and GDF-11 sequences  
 CC reveals potential N-linked glycosylation signals and putative  
 CC proteolytic processing sites at analogous positions. The 2  
 CC sequences are related not only in the C-terminal region following  
 CC the putative cleavage site (90% amino acid sequence identity) but  
 CC also in the pro-region of the molecules (45% amino acid sequence  
 CC identity. Claimed transgenic animals in which GDF-11 production is  
 CC reduced produce higher than normal levels of muscle and are useful  
 CC in the food industry. GDF-11 polypeptides, polynucleotides and  
 CC antibodies can be used to modulate GDF-11 activity or gene  
 CC expression for treatment of cell proliferative disorders involving  
 CC muscle, nerve and adipose tissue.

Sequence 375 AA:

Query Match 99.0%; Score 622; DB 19; Length 375;  
 Best Local Similarity 99.1%; Pred. No. 5.1e-59;  
 Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFGLDDEHSTESRCRRYPLTVDFEAFGMDWIAPRKRYKANVCSGCEPFVLOKYPHTL 60  
 Db 267 dfgldcdenstescrrcrrypltvdfefgwdwliaprrykanvcsgecefvlqkyphtl 326  
 OY 61 VHOANPRGSAGPCCPTPLMSPIMLYFNKGKQIITYGKIPAMVVDRCGCS 109  
 Db 327 vhoanprgsagpccptplmspimlmyfnkgkqilygkipamvvdrcgcs 375

Search completed: May 20, 2002, 09:21:47  
 Job time: 82 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 20, 2002, 09:20:25 ; Search time 13.12 Seconds  
(without alignments)  
202.926 Million cell updates/sec

Title: US-09-754-826-2

Perfect score: 628

Sequence: 1 DFGLDCEHSTESRCRYPL.....KEQIYKIPAMVDRGCS 109

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents\_AA:\*

2: /cgn2\_6/prodata/2/1aa/5a\_COMB.pep:\*

3: /cgn2\_6/prodata/2/1aa/5b\_COMB.pep:\*

4: /cgn2\_6/prodata/2/1aa/5a\_COMB.pep:\*

5: /cgn2\_6/prodata/2/1aa/5b\_COMB.pep:\*

6: /cgn2\_6/prodata/2/1aa/5b\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	99.0	126	2	US-08-525-596B-6
2	622	99.0	126	3	US-09-177-860A-6
3	622	99.0	126	2	US-08-525-596B-14
4	622	99.0	375	2	US-08-765-875-5
5	622	99.0	375	3	US-08-765-875-5
6	622	99.0	375	3	US-09-177-860A-14
7	622	99.0	376	3	US-08-525-596B-12
8	622	99.0	376	3	US-09-177-860A-12
9	622	99.0	376	3	US-08-891-789B-6
10	611	97.3	375	3	US-08-891-789B-2
11	583	92.8	108	2	US-08-525-596B-8
12	583	92.8	108	3	US-09-177-860A-8
13	574	91.4	126	1	US-08-247-907A-2
14	574	91.4	126	1	US-08-452-772-2
15	574	91.4	126	3	US-08-765-875-4
16	574	91.4	126	3	US-08-795-671-4
17	574	91.4	126	4	US-09-414-234-2
18	574	91.4	126	5	PCT-US94-05288-2
19	574	91.4	362	1	US-08-247-907A-11
20	574	91.4	362	1	US-08-452-772-11
21	574	91.4	362	4	US-09-414-234-11
22	574	91.4	362	4	PCT-US94-05288-11
23	574	91.4	407	2	US-08-765-875-2
24	574	91.4	407	2	US-08-765-875-6
25	574	91.4	407	3	US-08-795-671-2
26	574	91.4	407	3	US-08-795-671-6
27	256	40.8	52	1	US-08-247-907A-4

28	256	40.8	52	1	US-08-452-772-4	Sequence 4, Appl1
29	256	40.8	52	4	US-09-414-234-4	Sequence 4, Appl1
30	256	40.8	52	5	PCT-US94-05288-4	Sequence 12, Appl1
31	241	38.4	128	1	US-08-455-550-12	Sequence 37, Appl1
32	235	37.4	115	1	US-08-197-792-37	Sequence 37, Appl1
33	235	37.4	115	1	US-08-459-850-37	Sequence 37, Appl1
34	235	37.4	115	1	US-08-459-850-37	Sequence 37, Appl1
35	235	37.4	120	1	US-08-481-377-22	Sequence 22, Appl1
36	235	37.4	120	2	US-08-491-835-20	Sequence 20, Appl1
37	235	37.4	120	3	US-09-153-738A-22	Sequence 22, Appl1
38	235	37.4	120	3	US-08-946-092A-20	Sequence 20, Appl1
39	235	37.4	120	4	US-09-172-062-20	Sequence 20, Appl1
40	235	37.4	120	4	US-08-624-635-20	Sequence 20, Appl1
41	235	37.4	120	5	PCT-US94-00666-22	Sequence 22, Appl1
42	235	37.4	120	5	PCT-US94-00666-22	Sequence 22, Appl1
43	235	37.4	121	1	US-08-581-529B-18	Sequence 18, Appl1
44	235	37.4	121	1	US-08-455-559-24	Sequence 24, Appl1
45	235	37.4	121	2	US-08-525-596B-28	Sequence 28, Appl1

## ALIGNMENTS

RESULT 1  
US-08-525-596B-6  
Sequence 67, Application US/08525596B  
Patent No. 5827733  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525, 596B  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D, John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07265/075001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-08-525-596B-6,  
Query Match 99.0%; Score 622; DB 2; Length 126;  
Best Local Similarity 99.1%; Pred. No. 3.3e-66;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DFGLDCEHSTESRCRYPLTVDFEAGGMDWIIPKRYKANYCSGCECFVLRKYPHTL 60

Db 18 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 77  
OY 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109  
Db 78 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 126

RESULT 2  
US-09-177-860A-6  
Sequence 6, Application US/09177860A  
Patent No. 6096506  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-Jin  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-177-860A-6

Query Match 99.0%; Score 622; DB 3; Length 126;  
Best Local Similarity 99.1%; Pred. No. 3.3e-66;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 60  
Db 18 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 77  
OY 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109  
Db 78 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 126  
RESULT 3  
US-08-525-596B-14  
Sequence 14, Application US/08525596B  
Patent No. 5827733  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525,596B  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D, John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07265/075001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5099  
TELEFAX: 619-678-5070  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-525-596B-14

Query Match 99.0%; Score 622; DB 2; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 60  
Db 267 DFGDCCDHSTESRCCRYPLTVDFEAFGMDWIIAARKRYKANCSGECEVFLOKYPHTL 326  
OY 61 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 109  
Db 327 VHOANPRGSAGPCCTPTLMSPIINMLYFNKGEOIIGKIPAMVYDRCGCS 375  
RESULT 4  
US-08-765-875-5  
Sequence 5, Application US/08765875  
Patent No. 5914234  
GENERAL INFORMATION:  
APPLICANT: LEE, SE-JIN  
APPLICANT: MCPHERSON, ALEXANDRA C.  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,875  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,958  
FILING DATE:  
APPLICATION NUMBER: US/08/272,763  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: TUMARKIN PH.D., LISA A.  
REGISTRATION NUMBER: P-38,347  
REFERENCE/DOCKET NUMBER: PD3641  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/455-5100  
TELEFAX: 619/455-5110  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: GDF-8  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..375  
US-08-765-875-5

Query Match 99.0%; Score 622; DB 2; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCEHSTESRCRYPLTVDFEARGWMIAPKRYKANYCGEGEFVFLQKYPHTL 60  
DB 267 DFGIDCEHSTESRCRYPLTVDFEARGWMIAPKRYKANYCGEGEFVFLQKYPHTL 326  
QY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVRGCGS 109  
DB 327 VHOANPRGSAGPCCPTPKMSPINMLYFNKGKQIITGKIPANVVRGCGS 375

RESULT 5  
US-08-795-671-5  
Sequence 5, Application US/08795671  
Patent No. 6008434  
GENERAL INFORMATION:  
APPLICANT: Se-Jin Lee and Alexandra McPherron  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,671  
FILING DATE: February 6, 1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: HATTE, PH.D., LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/106001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: GDF-8  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..375  
US-08-795-671-5

Query Match 99.0%; Score 622; DB 3; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCEHSTESRCRYPLTVDFEARGWMIAPKRYKANYCGEGEFVFLQKYPHTL 60  
DB 267 DFGIDCEHSTESRCRYPLTVDFEARGWMIAPKRYKANYCGEGEFVFLQKYPHTL 326  
QY 61 VHOANPRGSAGPCCPTPLMSPINMLYFNKGKQIITGKIPANVVRGCGS 109  
DB 327 VHOANPRGSAGPCCPTPKMSPINMLYFNKGKQIITGKIPANVVRGCGS 375

RESULT 6  
US-09-177-860A-14  
Sequence 14, Application US/09177860A  
Patent No. 6096506  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: HATTE, PH.D., LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-09-177-860A-14

Query Match 99.0%; Score 622; DB 3; Length 375;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 60  
Db 267 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 326  
Qy 61 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 109  
Db 327 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 375

RESULT 7  
US-08-525-596B-12  
; Sequence 12, Application US/08525596B  
; Patent No. 5827733

GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525,596B  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07265/075001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-525-596B-12

Query Match 99.0%; Score 622; DB 2; Length 376;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 60  
Db 268 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 327  
Qy 61 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 109  
Db 328 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 376

RESULT 8

US-09-177-860A-12  
; Sequence 12, Application US/09177860A  
; Patent No. 6096506

GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-jin  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-177-860A-12

Query Match 99.0%; Score 622; DB 3; Length 376;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 60  
Db 268 DFGDDEHSTESRCRCRYPLTVDFEAFGMDWIIAPKRYKANCSCGCEVFLOKYPHTL 327  
Qy 61 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 109  
Db 328 VHQANPRGSAGPCCTPTLMSPINMLYFNKGEOIYYKIKIPAMVYDRGCS 376

RESULT 9  
US-08-891-789B-6  
; Sequence 6, Application US/08891789B  
; Patent No. 6103466

GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel  
TITLE OF INVENTION: Double-Muscling in Mammals  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
ZIP: M5L 1A9  
COUNTRY: Canada  
COMPUTER READABLE FORM:

4 MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,789B  
FILING DATE: July 14, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 52836/00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-891-789B-6

Query Match 99.0%; Score 622; DB 3; Length 376;  
Best Local Similarity 99.1%; Pred. No. 1.2e-65;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 60  
|||||  
Db 268 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 327  
QY 61 VHQANPRGSAGPCCPTPLMSPINMLYFNKGEOIILYGRIPAMVVDRCGS 109  
|||||  
Db 328 VHQANPRGSAGPCCPTPKMSPINMLYFNKGEOIILYGRIPAMVVDRCGS 376

RESULT 10  
US-08-891-789B-2  
Sequence 2, Application US/08891789B  
Patent No. 6103466  
GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel  
TITLE OF INVENTION: Double-Muscling in Mammals  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
ZIP: M5L 1A9  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,789B  
FILING DATE: July 14, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 52836/00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-891-789B-2

Query Match 97.3%; Score 611; DB 3; Length 375;  
Best Local Similarity 97.2%; Pred. No. 2.4e-64;  
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 60  
|||||  
Db 267 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 326  
QY 61 VHQANPRGSAGPCCPTPLMSPINMLYFNKGEOIILYGRIPAMVVDRCGS 109  
|||||  
Db 327 VHQANPRGSAGPCCPTPKMSPINMLYFNKGEOIILYGRIPAMVVDRCGS 375

RESULT 11  
US-08-525-596B-8  
Sequence 8, Application US/08525596B  
Patent No. 5827733  
GENERAL INFORMATION:

APPLICANT: Huyhn, Thanh  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/525,596B  
FILING DATE: 19-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07762  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D, John R.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: 07265/075001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-525-596B-8

Query Match 92.8%; Score 583; DB 2; Length 108;  
Best Local Similarity 99.0%; Pred. No. 1.1e-61;  
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 60  
|||||  
Db 6 DFGIDCDHEHSTESRCRCRYPLTVDEAFGWMIIAPKRYKANYCGEGEFVLOKYPHTL 65  
QY 61 VHQANPRGSAGPCCPTPLMSPINMLYFNKGEOIILYGRIPAMV 103  
|||||  
Db 66 VHQANPRGSAGPCCPTPKMSPINMLYFNKGEOIILYGRIPAMV 108

RESULT 12  
US-09-177-860A-8  
Sequence 8, Application US/09177860A  
Patent No. 6096506  
GENERAL INFORMATION:  
APPLICANT: Huynh, Thanh  
APPLICANT: Lee, Se-Jin  
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gray Cary Ware & Freidenrich LLP  
STREET: 4365 Executive Drive, Suite 1600  
CITY: San Diego  
STATE: CA  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/177,860A  
FILING DATE: 23-OCT-1998  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/525,596  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D. Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/075003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 858-677-1456  
TELEFAX: 858-677-1465  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal  
US-09-177-860A-8

Query Match 92.8%; Score 583; DB 3; Length 108;  
Best Local Similarity 99.0%; Pred. No. 1.1e-61;  
Matches 102; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGLDGDHSTSRCCRYPLTVDFEAFGMDWIAPRRKRYANCSGCEVFLOKIPHTL 60  
|||||  
6 DGLDGDHSTSRCCRYPLTVDFEAFGMDWIAPRRKRYANCSGCEVFLOKIPHTL 65  
|||||

DB 61 VQANPRGSAGPCPTLMSPINMLYFNKGEOIYGIKIPAMV 103  
|||||  
66 VQANPRGSAGPCPTLMSPINMLYFNKGEOIYGIKIPAMV 108  
|||||

RESULT 13  
US-08-247-907A-2  
Sequence 2, Application US/08247907A  
Patent No. 5639638-  
GENERAL INFORMATION:  
APPLICANT: WOZNEY, John  
APPLICANT: CELESTE, Anthony J.  
TITLE OF INVENTION: BMP-11 COMPOSITIONS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENETICS INSTITUTE, INC.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA

ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/247,907A  
FILING DATE: May 20, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LAZAR, Steven R.  
REGISTRATION NUMBER: 32,618  
REFERENCE/DOCKET NUMBER: G15205-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617 876-1170  
TELEFAX: 617 876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 126 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-247-907A-2

Query Match 91.4%; Score 574; DB 1; Length 126;  
Best Local Similarity 89.0%; Pred. No. 1.5e-60;  
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 DGLDGDHSTSRCCRYPLTVDFEAFGMDWIAPRRKRYANCSGCEVFLOKIPHTL 60  
|||||  
DB 18 NLGDDHSSSRCCRYPLTVDFEAFGMDWIAPRRKRYANCSGCEVFLOKIPHTL 77  
|||||

QY 61 VQANPRGSAGPCPTLMSPINMLYFNKGEOIYGIKIPAMVDRGCS 109  
|||||  
DB 78 VQANPRGSAGPCPTLMSPINMLYFNKGEOIYGIKIPAMVDRGCS 126  
|||||

RESULT 14  
US-08-452-772-2  
Sequence 2, Application US/08452772  
Patent No. 5700911  
GENERAL INFORMATION:  
APPLICANT: WOZNEY, John  
APPLICANT: CELESTE, Anthony J.  
TITLE OF INVENTION: BMP-11 COMPOSITIONS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENETICS INSTITUTE, INC.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,772  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/247,907  
FILING DATE: 20-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: LAZAR, Steven R.  
REGISTRATION NUMBER: 32,618  
REFERENCE/DOCKET NUMBER: G15205-CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617 876-1170



